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OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:48:34 ; Search time 106.452 Seconds
(without alignments)
4565.212 Million cell updates/sec

Title: us-10-079-954-1
Perfect score: 297
Sequence: 1 gcaatcgatggggatcctt.....ccatcaagaagattatggt 297

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	3	US-09-308-984-1
2	282.8	95.2	933	3	US-08-808-148-2
3	282.8	95.2	1289	3	US-09-020-956-111
4	282.8	95.2	1289	3	US-09-030-607-111
5	282.8	95.2	1289	3	US-09-439-313-111
6	282.8	95.2	1289	3	US-09-352-616A-111
7	282.8	95.2	1289	3	US-09-232-149A-111
8	282.8	95.2	1289	4	US-09-159-812-111
9	282.8	95.2	1289	4	US-09-636-215-111
10	282.8	95.2	1289	4	US-09-685-166A-111
11	282.8	95.2	1289	4	US-09-115-453-111
12	282.8	95.2	1289	4	US-09-688-489-111
13	282.8	95.2	1289	4	US-09-679-426-111
14	282.8	95.2	1289	4	US-09-759-143-111
15	282.8	95.2	1289	4	US-09-651-236-111
16	282.8	95.2	1324	4	US-09-148-545-82
17	282.8	95.2	1376	4	US-09-148-545-14
18	272.8	91.9	740	3	US-09-020-956-17
19	272.8	91.9	740	3	US-09-030-607-17
20	272.8	91.9	740	3	US-09-439-313-17
21	272.8	91.9	740	3	US-09-352-616A-17
22	272.8	91.9	740	3	US-09-232-149A-17
23	272.8	91.9	740	4	US-09-159-812-17
24	272.8	91.9	740	4	US-09-636-215-17
25	272.8	91.9	740	4	US-09-685-166A-17
26	272.8	91.9	740	4	US-09-115-453-17
27	272.8	91.9	740	4	US-09-688-489-17

28	272.8	91.9	740	4	US-09-679-426-17	Sequence 17, Appl
29	272.8	91.9	740	4	US-09-759-143-17	Sequence 17, Appl
30	272.8	91.9	740	4	US-09-651-236-17	Sequence 17, Appl
31	263.8	88.8	729	3	US-09-020-956-13	Sequence 13, Appl
32	263.8	88.8	729	3	US-09-030-607-13	Sequence 13, Appl
33	263.8	88.8	729	3	US-09-439-313-13	Sequence 13, Appl
34	263.8	88.8	729	3	US-09-352-616A-13	Sequence 13, Appl
35	263.8	88.8	729	3	US-09-232-149A-13	Sequence 13, Appl
36	263.8	88.8	729	4	US-09-159-812-13	Sequence 13, Appl
37	263.8	88.8	729	4	US-09-636-215-13	Sequence 13, Appl
38	263.8	88.8	729	4	US-09-685-166A-13	Sequence 13, Appl
39	263.8	88.8	729	4	US-09-115-453-13	Sequence 13, Appl
40	263.8	88.8	729	4	US-09-688-489-13	Sequence 13, Appl
41	263.8	88.8	729	4	US-09-679-426-13	Sequence 13, Appl
42	263.8	88.8	729	4	US-09-759-143-13	Sequence 13, Appl
43	263.8	88.8	729	4	US-09-651-236-13	Sequence 13, Appl
C 44	220.6	74.3	801	3	US-09-020-956-16	Sequence 16, Appl
C 45	220.6	74.3	801	3	US-09-030-607-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-308-984-1
; Sequence 1, Application US/09308984
; Patent No. 6388065
; GENERAL INFORMATION:
; APPLICANT: Durst, Matthias
; APPLICANT: Nees, Matthias
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09902857)
; CURRENT APPLICATION NUMBER: US/09/308,984
; CURRENT FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/DE97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-308-984-1

Query Match 100.0%; Score 297; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.4e-79;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAG	60
Db	1	GCAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAG	60
Qy	61	TTTGTCAACGTGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTCTTGGTTTC	120
Db	61	TTTGTCAACGTGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTCTTGGTTTC	120
Qy	121	CTGGGCTGCTATGCTGTCTAAGACTGAGCAAGTGTGCGCTCGTGAGGTTCTTCTTCATC	180
Db	121	CTGGGCTGCTATGCTGTCTAAGACTGAGCAAGTGTGCGCTCGTGAGGTTCTTCTTCATC	180
Qy	181	CTCTCTCTCATCTTCATTGCTGAGTTGTCAGTCTGCTGGTTCGCTTGGTGACACCATTA	240
Db	181	CTCTCTCTCATCTTCATTGCTGAGTTGTCAGTCTGCTGGTTCGCTTGGTGACACCATTA	240
Qy	241	ATGGCTGAGCACTTCCGAGGTTGCTGCTAGTGTGCTGCCATCAAGAAGATTATGTTT	297
Db	241	ATGGCTGAGCACTTCCGAGGTTGCTGCTAGTGTGCTGCCATCAAGAAGATTATGTTT	297

RESULT 2
US-08-808-148-2
; Sequence 2, Application US/08808148

BEST AVAILABLE COPY

NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
DB 220 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 121
DB 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 339
QY 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 181
DB 340 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 399
QY 182 TCCTCTCATCTTCATTTGCTGAGTGTGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 241
DB 400 TCCTCTCATCTTCATTTGCTGAGTGTGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 459
QY 242 TGGGCTGAGCACTTCCGAGCGTTGCTGGTAGTGCCTGCGCATCAAGAA 287
DB 460 TGGGCTGAGCACTTCCGAGCGTTGCTGGTAGTGCCTGCGCATCAAGAA 505

RESULT 5
US-09-439-313-111
; Sequence 111, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary

APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 111
LENGTH: 1289
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
DB 220 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 121
DB 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 339
QY 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 181
DB 340 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 399
QY 182 TCCTCTCATCTTCATTTGCTGAGTGTGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 241
DB 400 TCCTCTCATCTTCATTTGCTGAGTGTGAGCAAGTGTGCCCTCGTGAGCGTTCTTCTTCATCC 459
QY 242 TGGGCTGAGCACTTCCGAGCGTTGCTGGTAGTGCCTGCGCATCAAGAA 287
DB 460 TGGGCTGAGCACTTCCGAGCGTTGCTGGTAGTGCCTGCGCATCAAGAA 505

RESULT 6
US-09-352-616A-111
; Sequence 111, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
DB 220 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGCTCTTGGTTTCC 121

Qy	2	CAATCATGGGCATCCTTTTCTGAAGATCTTCGGGCGACTGTGTCGACGTGCCATGCAGT	61
Db	220	CAATCATGGGCATCCTTTTCTGAAGATCTTCGGGCGCGCTGTGTCGACGTGCCATGCAGT	279
Qy	62	TTGTCAACGTGGGCTACTTCCCTCATCGACGCGGGCTTGTGGTCTTTTGCTCTTGTTTTC	121
Db	280	TTGTCAACGTGGGCTACTTCCCTCATCGACGCGGGCTTGTGGTCTTTTGCTCTTGTTTTC	339
Qy	122	TGGGCTGCTATGGTGTCTAAGA CTGAGAGCAAGTGTGCCCTCGTGACGCTTCTTTCATCC	181
Db	340	TGGGCTGCTATGGTGTCTAAGA CTGAGAGCAAGTGTGCCCTCGTGACGCTTCTTTCATCC	399
Qy	182	TCCTCCTCATCTTCATGCTGAGGTTGCAGCTGCTGTGTGCGCTTCGTGTACACCATAA	241
Db	400	TCCTCCTCATCTTCATGCTGAGGTTGCAGCTGCTGTGTGCGCTTCGTGTACACCATAA	459
Qy	242	TGCGTGAGCACTCCGACGTTGCTGGTAGTGCCTTGCCATCAAGAA	287
Db	460	TGCGTGAGCACTCTCGACGTTGCTGGTAGTGCCTTGCCATCAAGAA	505

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RESULT 10
US-09-685-166A-111
; Sequence 111, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF DISEASES
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FaetSEQ for Windows Version 1.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homb sapien
US-09-685-166A-111

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Query Match	95.2%;	Score 282.8;	DB 4;	Length 1289;
Best Local Similarity	99.3%;	Pred. No. 8e-75;		
Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	2	CAATCGATGGGCATCTTTTCTGAAGATCTTCGGGCCACTGTCTCGAGTCCATGCAGT	61	
DB	220	CNATCGATGGGCATCTTTTCTGAAGATCTTCGGGCCACTGTCTCGAGTCCATGCAGT	279	
QY	62	TTGTCAAGTGGGGTACTTTCTTCATCGACGGCGTGTGGTCTTTGGCTCTTGGTTTC	121	
DB	280	TTGTCAAGCTGGGGTACTTTCTTCATCGACGGCGTGTGGTCTTTGGCTCTTGGTTTC	339	
QY	122	TGGGCTCTATGGTGCTTAAGACTCAGAGCAAGTGTGCCCTCGTCACTTCTTTTCATCC	181	
DB	340	TGGGCTCTATGGTGCTTAAGACTCAGAGCAAGTGTGCCCTCGTCACTTCTTTTCATCC	399	
QY	182	TCCTCTCATCTTTCATTGTCTGAGGTTGCAGTCTGTGGTGCCTCTGGGTACACCAATAA	241	

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Db      400  TCTCTCTCATCTTCATTGCTCTGAGGTTCGAGCTGCTGTGGTTCGCGCTTGGGTATACACCACAA 459
QY      242  TGGCTGAGCAGCTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 287
Db      460  TGGCTGAGCAGCTTCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 505

RESULT 11
US-09-115-453-111
; Sequence 111, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-111

Query Match 95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      2  CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACCTGCTCCAGTGCCATGCAGT 61
Db      220  CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACCTGCTCCAGTGCCATGCAGT 279

QY      62  TTGTCAACGTGGGCTACTCTTCATATCGACGCGCGTGTGGTCTTTGCTCTTGGTTTCC 121
Db      280  TTGTCAACGTGGGCTACTCTTCATATCGACGCGCGTGTGGTCTTTGCTCTTGGTTTCC 339

QY      122  TGGGCTGCTATGGTCTTAAGACTCAGAGCAAGTGTGCCCTCGTGAGGTCTTCTTCATCC 181
Db      340  TGGGCTGCTATGGTCTTAAGACTCAGAGCAAGTGTGCCCTCGTGAGGTCTTCTTCATCC 399

QY      182  TCTCTCTCATCTTTCATTGCTGAGGTTCGAGCTGCTGTGGTTCGCTTGGTGTACACCATAA 241
Db      400  TCTCTCTCATCTTTCATTGCTGAGGTTCGAGCTGCTGTGGTTCGCTTGGTGTACACCACAA 459

QY      242  TGGCTGAGCAGCTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 287
Db      460  TGGCTGAGCAGCTTCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 505

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RESULT 12
US-09-688-489-111
; Sequence 111, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-111

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RESULT 15

US-09-651-236-111
; Sequence 111, Application US/09651236
; Patent No. 6818751

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-111

Query Match 95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	2	CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGATGCACT 61
Db	220	CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCGATGCACT 279
QY	62	TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGGCTTGGTCTTTGGTCTTTGGTTTCC 121
Db	280	TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGGCTTGGTCTTTGGTCTTTGGTTTCC 339
QY	122	TGGGCTGTCTATGGTGTAAAGACTGAGACAAAGTGCCTCGTGACGTTCTTCTTCATCC 181
Db	340	TGGGCTGTCTATGGTGTAAAGACTGAGACAAAGTGCCTCGTGACGTTCTTCTTCATCC 399
QY	182	TCTCTCTCATCTTTCATGTGTAGGTTGACAGTGTGTGTGCTGTGTGCTTGGTGTACACATAA 241
Db	400	TCTCTCTCATCTTTCATGTGTAGGTTGACAGTGTGTGTGCTGTGTGCTTGGTGTACACACAA 459
QY	242	TGGCTGAGCAGTCCCGAGCTTCTGCTAGTGCCTGCCATCAAGAA 287
Db	460	TGGCTGAGCAGTCCCGAGCTTCTGCTAGTGCCTGCCATCAAGAA 505

Search completed: August 27, 2005, 11:37:05
Job time : 107.452 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 07:00:48 ; Search time 355.016 Seconds
(without alignments)
4952.347 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 297

Sequence: 1 gcaatcgatggggcattcctt.....ccatcaagaagattatgggt 297

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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- 2: Geneseqn1990s:*
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- 4: Geneseqn2001as:*
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- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	2	AAV15588 Human HPK
2	282.8	95.2	513	5	AAf93382 Lung carc
3	282.8	95.2	635	4	AAI29471 Colon tum
4	282.8	95.2	635	8	ABZ33657 Human col
5	282.8	95.2	792	6	ABK29835 Colon ade
6	282.8	95.2	933	2	AAV54014 Nucleotid
7	282.8	95.2	1076	6	ABS76533 cDNA enco
8	282.8	95.2	1076	10	ADB75600 Prostate
9	282.8	95.2	1076	13	ADR25330 Breast ca
10	282.8	95.2	1076	13	ADR65868 Human pro
11	282.8	95.2	1076	13	ADR66771 Human tum
12	282.8	95.2	1077	13	Adq85081 Human tum
13	282.8	95.2	1154	6	ABS76532 cDNA enco
14	282.8	95.2	1154	10	ADB75598 Prostate
15	282.8	95.2	1278	11	ADN39285 Cancer/an
16	282.8	95.2	1288	2	AAV48113 Nucleotid
17	282.8	95.2	1288	10	AD62626 DNA #4 us
18	282.8	95.2	1288	10	AD62609 Human rec
19	282.8	95.2	1289	2	AAV58587 Prostate
20	282.8	95.2	1289	2	AAV61202 Full leng

21	282.8	95.2	1289	3	ABS71255 Human pro
22	282.8	95.2	1289	4	AAh93466 Human pro
23	282.8	95.2	1289	4	AAg63358 Human pro
24	282.8	95.2	1289	4	AAh02531 Prostate
25	282.8	95.2	1289	4	AAH84780 Human pro
26	282.8	95.2	1289	4	AAf86954 Human P50
27	282.8	95.2	1289	5	ACA59367 Prostate
28	282.8	95.2	1289	5	AAg10109 Human pro
29	282.8	95.2	1289	6	ABL94930 Human NI-
30	282.8	95.2	1289	6	ABS58639 Prostate
31	282.8	95.2	1289	8	ACC95094 Prostate
32	282.8	95.2	1289	10	ADB13561 Human pro
33	282.8	95.2	1289	10	ADG25977 Human pro
34	282.8	95.2	1290	3	AAA06350 Human imm
35	282.8	95.2	1306	13	ADR44012 Human bre
36	282.8	95.2	1324	2	AAV34225 Human sec
37	282.8	95.2	1324	8	ACD08096 cDNA enco
38	282.8	95.2	1376	2	AAV34157 Human sec
39	282.8	95.2	1376	8	ACD08028 cDNA enco
40	282.8	95.2	1456	9	ADA11015 Human cDN
41	282.8	95.2	1533	3	AAZ95011 Cancer sp
42	282.8	95.2	1603	5	ABV23358 Human pro
43	282.8	95.2	1603	5	ADL62990 Human ova
44	282.8	95.2	1605	2	AAV30916 Human sec
45	282.8	95.2	1605	5	AAf98395 Human cDN

ALIGNMENTS

RESULT 1

AAV15588
ID AAV15588 standard; DNA; 297 BP.

XX AAV15588;

XX 02-JUL-1998 (first entry)

XX Human HPK-1A C4.8 DNA.

XX Cervical cancer; treatment; diagnosis; passage cell; lesion;

XX human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

XX Homo sapiens.

XX DE19649207-C1.

XX 26-FEB-1998.

XX 27-NOV-1996; 96DE-01049207.

XX 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Duerst M, Nees M;

XX WPI; 1998-121623/12.

XX P-P5DB; AAW47275.

XX Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for progression of cervical lesions.

XX Claim 2; Fig 1; 8pp; German.

XX This sequence, C4.8, is derived from a human papillomavirus (HPV)

XX immortalised human foreskin keratinocyte cell line HPK-1A and is characteristic of late or early passage cells. This sequence is used in a method for assessing the potential for progression of cervical lesions. Antibodies generated against the encoded polypeptide are used for diagnosis of cervical cancer and to assess potential for lesion

CC progression. Antibodies can also be used therapeutically by inhibiting
CC the polypeptide. Antisense molecules based on the nucleotide sequence are
CC used to inhibit expression of the protein. Detecting polypeptides, or
CC related RNA, characteristic of late passage cells (which are potentially
CC malignant) in cervical smears is a reliable way of assessing progression
CC potential
XX
SQ Sequence 297 BP; 46 A; 79 C; 80 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 297; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 4.5e-76;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCCTCCAGTGCCATGCAG 60
Db 1 GCAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCCTCCAGTGCCATGCAG 60
QY 61 TTTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTCTGGTTTC 120
Db 61 TTTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTCTGGTTTC 120
QY 121 CTGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
Db 121 CTGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
QY 181 CTCCTCCTCATCTTCATTCGTGAGGTTCAGTGTGCTGTGCTTGGTGTACACCATTA 240
Db 181 CTCCTCCTCATCTTCATTCGTGAGGTTCAGTGTGCTGTGCTTGGTGTACACCATTA 240
QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTGAGTGCCTGCGCATCAAGAAGATTATGGTT 297
Db 241 ATGGCTGAGCACTTCCCGACGTTGCTGTGAGTGCCTGCGCATCAAGAAGATTATGGTT 297

RESULT 2
AAF93382
ID AAF93382 standard; cDNA; 513 BP.
XX
AC AAF93382;
XX
DT 21-MAY-2001 (first entry)
XX
DE Lung carcinoma cDNA encoding SRT protein SEQ ID 203.
XX
KW Human; SRT; gene therapy; gene mapping; tissue typing; ss.
XX
OS Homo sapiens,
PN WO200107611-A2.
PD 01-FEB-2001.
XX
PF 21-JUL-2000; 2000WO-US020006.
XX
PR 26-JUL-1999; 99US-0145701P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Wood WI;
XX
DR WPI; 2001-112729/12.
XX
PT New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT for production of recombinant SRT polypeptides, gene mapping, diagnosing
PT genetic disorders and for gene therapy.
XX
PS Claim 2; Fig 203; 663pp; English.
XX

CC Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC human SRT proteins. The cDNA references are isolated from various
CC different human tissue cDNA libraries. The invention relates to a method
CC for detecting cDNA encoding an SRT protein, a vector containing cDNA
CC encoding SRT, a host cell transformed with the vector, an isolated SRT

CC polypeptide, and an antibody which binds to SRT. The polynucleotide
CC sequence can be used in gene therapy and is useful in the recombinant
CC production of SRT polypeptides, as a hybridisation probe to screen
CC libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC map the gene encoding the SRT polypeptides and analysing genetic
CC disorders, tissue typing and disease tissue detection. The SRT
CC polynucleotide sequences can be used in polymerase chain reaction,
CC screening for new therapeutic molecules and generation of antisense RNA
CC and DNA
XX
SQ Sequence 513 BP; 97 A; 135 C; 129 G; 152 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 5; Length 513;
Best Local Similarity 99.3%; Pred. No. 7.2e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCCTCCAGTGCCATGCAGT 61
Db 99 CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCCTCCAGTGCCATGCAGT 158
QY 62 TTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTGGTTTC 121
Db 159 TTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTGGTTTC 218
QY 122 TGGGCTGCTATGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 219 TGGGCTGCTATGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 278
QY 182 TCCTCCTCATCTTCATTCGTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATAA 241
Db 279 TCCTCCTCATCTTCATTCGTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCATAA 338
QY 242 TGGCTGAGCACTTCCCGACGTTGCTGTGAGTGCCTGCGCATCAAGAA 287
Db 339 TGGCTGAGCACTTCCCGACGTTGCTGTGAGTGCCTGCGCATCAAGAA 384

RESULT 3
AAI29471/c
ID AAI29471 standard; cDNA; 635 BP.
XX
AC AAI29471;
XX
DT 12-OCT-2001 (first entry)
XX
DE Colon tumour related determined cDNA sequence for clone R098:F06.
XX
KW Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
KW gene therapy; vaccine; colonic cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200149716-A2.
XX
PD 12-JUL-2001.
XX
PF 29-DEC-2000; 2000WO-US035596.
XX
PR 30-DEC-1999; 99US-00476296.
PR 10-JAN-2000; 2000US-00480321.
PR 15-FEB-2000; 2000US-00504629.
PR 06-MAR-2000; 2000US-00519444.
PR 19-MAY-2000; 2000US-00575251.
PR 29-JUN-2000; 2000US-00609448.
PR 28-AUG-2000; 2000US-00649811.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI King GE, Wang T, Jiang Y;
XX
DR WPI; 2001-441847/47.
XX

PT Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer.

XX Claim 2; Page 414; 472pp; English.

XX The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AA129460 to AA129512 and AA24494 to AA24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention

XX Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;

Query Match 95.2%; Score 282.8; DB 4; Length 635;

Best Local Similarity 99.3%; Pred. No. 7.8e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 61

Db 575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 516

QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGCTGCTCTTGGTTCCTTGGTTCC 121

Db 515 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGCTGCTCTTGGTTCCTTGGTTCC 456

QY 122 TGGGCTGCTATGCTGCTAGAGTTCGAGCAAGTGTCGCTCGTGCAGTTCCTTCTTCATCC 181

Db 455 TGGGCTGCTATGCTGCTAGAGTTCGAGCAAGTGTCGCTCGTGCAGTTCCTTCTTCATCC 396

QY 182 TCCTCCTCATCTTCATTTGCTGAGTTCGAGTTCGCTCGCTTGGTGTACACCAATAA 241

Db 395 TCCTCCTCATCTTCATTTGCTGAGTTCGAGTTCGCTCGCTTGGTGTACACCAATAA 336

QY 242 TGGCTGAGCACTTCCGAGTTCGCTGGTGTAGTTCGCTCGCATCAAGAA 287

Db 335 TGGCTGAGCACTTCCGAGTTCGCTGGTGTAGTTCGCTCGCATCAAGAA 290

RESULT 4

ABZ33657/c

ID ABZ33657 standard; cDNA; 635 BP.

XX ABZ33657;

XX ABZ33657;

DT 30-JAN-2003 (first entry)

XX Human colon tumour cDNA for clone R0098:F06 SEQ ID NO:1025.

DE Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;

KW tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200283070-A2.

PN

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US011475.

XX 10-APR-2001; 2001US-00833263.

PR 03-AUG-2001; 2001US-00922217.

PR 19-DEC-2001; 2001US-00025380.

XX (CORI-) CORIXA CORP.

PA

XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;

PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;

PI Fanger GR, Vedvick TS, Carter D;

XX WPI; 2003-067548/06.

DR

XX New polynucleotide, useful for the preparation of a composition for

PT stimulating an immune response against, or treating, cancer.

PT

PS Disclosure; Page 415; 537pp; English.

XX The present invention describes compounds (I) for the immunotherapy and

CC diagnosis of colon cancer. Also described: (1) a method for detecting the

CC presence of cancer in a patient; (2) a method for stimulating and/or

CC expanding T cells specific for a tumour protein; (3) an isolated T cell

CC population comprising T cells prepared by the method of (2); (4) a method

CC for stimulating an immune response in a patient; (5) a method for

CC treating cancer in a patient; and (6) a method for inhibiting the

CC development of cancer in a patient. (I) have immunostimulant and

CC cytostatic activities and can be used in vaccines. ABZ32646 to ABZ33725

CC and ABP55343 to ABP55391 represent human colon cancer/tumour related

CC sequences used in the exemplification of the present invention

CC

XX Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;

Query Match 95.2%; Score 282.8; DB 8; Length 635;

Best Local Similarity 99.3%; Pred. No. 7.8e-72;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 61

Db 575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCACT 516

QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGCTGCTCTTGGTTCCTTGGTTCC 121

Db 515 TTGTCAACGTGGGCTACTTCTCATCGACGCGCGCTTGCTGCTCTTGGTTCCTTGGTTCC 456

QY 122 TGGGCTGCTATGCTGCTAGAGTTCGAGCAAGTGTCGCTCGTGCAGTTCCTTCTTCATCC 181

Db 455 TGGGCTGCTATGCTGCTAGAGTTCGAGCAAGTGTCGCTCGTGCAGTTCCTTCTTCATCC 396

QY 182 TCCTCCTCATCTTCATTTGCTGAGTTCGAGTTCGCTCGCTTGGTGTACACCAATAA 241

Db 395 TCCTCCTCATCTTCATTTGCTGAGTTCGAGTTCGCTCGCTTGGTGTACACCAATAA 336

QY 242 TGGCTGAGCACTTCCGAGTTCGCTGGTGTAGTTCGCTCGCATCAAGAA 287

Db 335 TGGCTGAGCACTTCCGAGTTCGCTGGTGTAGTTCGCTCGCATCAAGAA 290

RESULT 5

ABK29835

ID ABK29835 standard; cDNA; 792 BP.

XX ABK29835;

XX ABK29835;

DT 23-APR-2002 (first entry)

XX Colon adenocarcinoma-specific cDNA #361.

DE Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.

XX

XX

QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGGTCTTTGCTTTGGTTTCC 121
 Db 285 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGGTCTTTGCTTTGGTTTCC 344
 QY 122 TGGGCTGCTATGGTGTAGACTGAGCAAGTGGCCCTCGTGAGCTTCTTTCATCC 181
 Db 345 TGGGCTGCTATGGTGTAGACTGAGCAAGTGGCCCTCGTGAGCTTCTTTCATCC 404
 QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATA 241
 Db 405 TCCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATA 464
 QY 242 TGCTGAGCACTTCCGACGTTGCTGTAGTGGCTGCCATCAAGAA 287
 Db 465 TGCTGAGCACTTCCGACGTTGCTGTAGTGGCTGCCATCAAGAA 510

RESULT 7
 ABS76533
 ID ABS76533 standard; cDNA; 1076 BP.
 XX
 AC ABS76533;
 XX
 DT 11-DEC-2002 (first entry)
 XX
 DE cDNA encoding human ovarian cancer marker M328.
 XX
 KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KW Central nervous system disorder; bacterial meningitis; viral meningitis;
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
 KW brain herniation; inflammation; encephalitis; testicular disorder;
 KW nontuberculous granulomatous orchitis; connective tissue disorder;
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
 KW histological type; carcinogenic; ovarian cancer marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200271928-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 14-MAR-2002; 2002WO-US007826.
 XX
 PR 14-MAR-2001; 2001US-0276025P.
 PR 14-MAR-2001; 2001US-0276026P.
 PR 10-AUG-2001; 2001US-0311732P.
 PR 19-SEP-2001; 2001US-0323580P.
 PR 26-SEP-2001; 2001US-0324967P.
 PR 26-SEP-2001; 2001US-0325102P.
 PR 26-SEP-2001; 2001US-0325149P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
 XX
 DR WPI: 2002-723277/78.
 DR P-PSDB; ABG96434.
 XX
 PT Assessing whether a patient is afflicted with ovarian cancer, useful in
 PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient.
 XX
 PS Disclosure; Page 445-446; 481pp; English.
 XX
 CC The present invention relates to a new method for assessing whether a
 CC patient is afflicted with ovarian cancer. The method involves comparing
 CC the expression level of a marker in a patient sample and the normal level
 CC of expression of the marker in a control non-ovarian cancer sample, where
 CC the marker is selected from 363 cancer markers described in the
 CC specification. The method of the invention is useful in diagnosing or

CC characterising cancer, in detecting the presence of cancer as early as
 CC possible, and the recurrence of ovarian cancer. The method may also be of
 CC particular use with patients having an enhanced risk of developing
 CC ovarian cancer (e.g. patients having a familial history of ovarian
 CC cancer). The cancer markers may be used in the management and treatment
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and
 CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
 CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
 CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
 CC testicular disorders (e.g. nontuberculous granulomatous orchitis),
 CC connective tissue disorders, or heart disorders (e.g. ischaemic heart
 CC disease or atherosclerosis). The compositions and methods may also be
 CC used in assessing the histological type of neoplasm associated with
 CC ovarian cancer, monitoring the progression of ovarian cancer, determining
 CC whether ovarian cancer has metastasized or is likely to metastasize,
 CC selecting a composition for inhibiting ovarian cancer, assessing the
 CC ovarian carcinogenic potential of a compound, or inhibiting ovarian
 CC cancer or at risk of developing ovarian cancer. The present nucleic acid
 CC sequence encodes one of the ovarian cancer markers described in the
 CC invention
 XX
 SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
 Query Match 95.2%; Score 282.8; DB 6; Length 1076;
 Best Local Similarity 99.3%; Pred. No. 9.4e-72;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAATCGATGGGCACTCTTCTGAAGATCTTGGGGCCACTGCTGCCAGTGCATGCAGT 61
 Db 98 CAATCGATGGGCACTCTTCTGAAGATCTTGGGGCCACTGCTGCCAGTGCATGCAGT 157
 QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGGTCTTTGCTTTGGTTTCC 121
 Db 158 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGGTCTTTGCTTTGGTTTCC 217
 QY 122 TGGGCTGCTATGGTGTAGACTGAGCAAGTGGCCCTCGTGAGCTTCTTTCATCC 181
 Db 218 TGGGCTGCTATGGTGTAGACTGAGCAAGTGGCCCTCGTGAGCTTCTTTCATCC 277
 QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATA 241
 Db 278 TCCTCTCATCTTCAATGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATA 337
 RESULT 8
 ADB75600
 ID ADB75600 standard; cDNA; 1076 BP.
 XX
 AC ADB75600;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Prostate cancer marker cDNA.
 XX
 KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003009814-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 25-JUL-2002; 2002WO-US023913.
 XX
 PR 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-0314356P.
 PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-0341746P.
 PR 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.
PA Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX WPI; 2003-248033/24.
XX New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
PT
XX Disclosure; SEQ ID NO 424; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 10; Length 1076;
Best Local Similarity 99.3%; Pred. No. 9.4e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 98 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGGCTTTGGTTTCC 121
DB 158 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGGCTTTGGTTTCC 217
QY 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGCCTCGTGAGCTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGCCTCGTGAGCTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCAATAA 241
DB 278 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCAATAA 337
QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTTGCCTGCCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTTGCCTGCCATCAAGAA 383

RESULT 9
ADR25330
ID ADR25330 standard; DNA; 1076 BP.
XX
AC ADR25330;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1191.
XX ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004065545-A2.
XX
PD 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.
PF
XX 15-JAN-2003; 2003US-00342887.
PR
XX (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
PA
XX Van't Veer LJ, He Y;
PI
XX WPI; 2004-593473/57.
DR
XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
XX Disclosure; SEQ ID NO 1191; 226pp; English.
XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 13; Length 1076;
Best Local Similarity 99.3%; Pred. No. 9.4e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 98 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGGCTTTGGTTTCC 121
DB 158 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGGCTTTGGTTTCC 217
QY 122 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGCCTCGTGAGCTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGCCTCGTGAGCTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCAATAA 241
DB 278 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCAATAA 337
QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTTGCCTGCCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTTGCCTGCCATCAAGAA 383

RESULT 10
ADR65868
ID ADR65868 standard; DNA; 1076 BP.
XX
AC ADR65868;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 64 #1.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX

CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
Query Match 95.2%; Score 282.8; DB 13; Length 1076;
Best Local Similarity 99.3%; Pred. No. 9.4e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCAATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 98 CAATCGATGGGCAATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157
QY 62 TTGTCAAGCTGGGCTACTTCTCATCGCAGCGGGGTTGTGCTTTGCTCTTGGTTTCC 121
DB 158 TTGTCAAGCTGGGCTACTTCTCATCGCAGCGGGGTTGTGCTTTGCTCTTGGTTTCC 217
QY 122 TGGGCTGCTATGCTGAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGCTGAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCATGCTGAGGTGTCAGCTGCTGTGTGTCGCTTGGTGACACCAATA 241
DB 278 TCCTCCTCATCTTCATGCTGAGGTGTCAGCTGCTGTGTGTCGCTTGGTGACACCAATA 337
QY 242 TGGCTGAGCACTTCGCGAGCTGCTGTGAGTGCCTGCTGCATCAAGAA 287
DB 338 TGGCTGAGCACTTCGCGAGCTGCTGTGAGTGCCTGCTGCATCAAGAA 383

RESULT 12

ADO85081

ID ADO85081 standard; cDNA; 1077 BP.

AC ADO85081;

DT 07-OCT-2004 (first entry)

DE Human tumour-associated antigenic target (TAT) cDNA sequence #1895.
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.OS

PN WO2004060270-A2.

PD 22-JUL-2004.

PF 15-OCT-2003; 2003WO-US029126.

PR 18-OCT-2002; 2002US-0418988P.

PA (GETH) GENENTECH INC.

PA (WUTD/) WU T D.

PA (ZHOU/) ZHOU Y.

PI Wu TD, Zhou Y;

DR WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 1895; 5504pp; English.
XX

CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX

SQ Sequence 1077 BP; 227 A; 279 C; 282 G; 289 T; 0 U; 0 Other;

Query Match

Best Local Similarity 95.2%; Score 282.8; DB 13; Length 1077;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCAATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 98 CAATCGATGGGCAATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157
QY 62 TTGTCAAGCTGGGCTACTTCTCATCGCAGCGGGGTTGTGCTTTGCTCTTGGTTTCC 121
DB 158 TTGTCAAGCTGGGCTACTTCTCATCGCAGCGGGGTTGTGCTTTGCTCTTGGTTTCC 217
QY 122 TGGGCTGCTATGCTGAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGCTGAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCATGCTGAGGTGTCAGCTGCTGTGTGTCGCTTGGTGACACCAATA 241
DB 278 TCCTCCTCATCTTCATGCTGAGGTGTCAGCTGCTGTGTGTCGCTTGGTGACACCAATA 337
QY 242 TGGCTGAGCACTTCGCGAGCTGCTGTGAGTGCCTGCTGCATCAAGAA 287
DB 338 TGGCTGAGCACTTCGCGAGCTGCTGTGAGTGCCTGCTGCATCAAGAA 383

RESULT 13

ABS76532

ID ABS76532 standard; cDNA; 1154 BP.

AC ABS76532;

XX

DT 11-DEC-2002 (first entry)

XX DE cDNA encoding human ovarian cancer marker M327.
 XX KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KW central nervous system disorder; bacterial meningitis; viral meningitis;
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
 KW brain herniation; inflammation; encephalitis; testicular disorder;
 KW non-tuberculous granulomatous orchitis; connective tissue disorder;
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
 KW histological type; carcinogenic; ovarian cancer marker; gene; ss.
 XX OS Homo sapiens.
 XX WO200271928-A2.
 XX PN 19-SEP-2002.
 XX PD 14-MAR-2002; 2002WO-US007826.
 XX PF 14-MAR-2001; 2001US-0276025P.
 XX PR 14-MAR-2001; 2001US-0276026P.
 XX PR 10-AUG-2001; 2001US-0311732P.
 XX PR 19-SEP-2001; 2001US-0323580P.
 XX PR 26-SEP-2001; 2001US-0324967P.
 XX PR 26-SEP-2001; 2001US-0325102P.
 XX PR 26-SEP-2001; 2001US-0325149P.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
 XX WPI: 2002-723277/78.
 DR P-PSDB; ABC96433.
 XX PT Assessing whether a patient is afflicted with ovarian cancer, useful in
 PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient.
 XX PS Disclosure; Page 444-445; 481pp; English.
 CC The present invention relates to a new method for assessing whether a
 CC patient is afflicted with ovarian cancer. The method involves comparing
 CC the expression level of a marker in a patient sample and the normal level
 CC of expression of the marker in a control non-ovarian cancer sample, where
 CC the marker is selected from 363 cancer markers described in the
 CC specification. The method of the invention is useful in diagnosing or
 CC characterising cancer, in detecting the presence of cancer as early as
 CC possible, and the recurrence of ovarian cancer. The method may also be of
 CC particular use with patients having an enhanced risk of developing
 CC ovarian cancer (e.g. patients having a familial history of ovarian
 CC cancer). The cancer markers may be used in the management and treatment
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and
 CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
 CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
 CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
 CC testicular disorders (e.g. non-tuberculous granulomatous orchitis),
 CC connective tissue disorders, or heart disorders (e.g. ischaemic heart
 CC disease or atherosclerosis). The compositions and methods may also be
 CC used in assessing the histological type of neoplasm associated with
 CC ovarian cancer, monitoring the progression of ovarian cancer, determining
 CC whether ovarian cancer has metastasized or is likely to metastasize,
 CC selecting a composition for inhibiting ovarian cancer, assessing the
 CC ovarian carcinogenic potential of a compound, or inhibiting ovarian
 CC cancer or at risk of developing ovarian cancer. The present nucleic acid
 CC sequence encodes one of the ovarian cancer markers described in the
 CC invention
 XX SQ Sequence 1154 BP; 307 A; 309 C; 255 G; 283 T; 0 U; 0 Other;
 Query Match 95.2%; Score 282.8; DB 6; Length 1154;

Best Local Similarity 99.3%; Pred. No. 9.7e-72;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CAATCATGGGCACTCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
 DB 221 CAATCATGGGCACTCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 280
 QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGTCTTGGTCTTTGGTCTTTGGTTTC 121
 DB 281 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGTCTTGGTCTTTGGTCTTTGGTTTC 340
 QY 122 TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGCCTCGTGCAGTCTTCTTTCATCC 181
 DB 341 TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGCCTCGTGCAGTCTTCTTTCATCC 400
 QY 182 TCCTCTCATCTTCATTGCTGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 DB 401 TCCTCTCATCTTCATTGCTGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460
 QY 242 TGGCTGAGCAGTTCGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
 DB 461 TGGCTGAGCAGTTCGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
 RESULT 14
 ADB75598
 ID ADB75598 standard; cDNA; 1154 BP.
 XX AC ADB75598;
 XX DT 04-DEC-2003 (first entry)
 XX DE Prostate cancer marker cDNA.
 XX KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
 OS Homo sapiens.
 XX WO2003009814-A2.
 XX PD 06-FEB-2003.
 XX PF 25-JUL-2002; 2002WO-US023913.
 XX PR 25-JUL-2001; 2001US-0307982P.
 XX PR 22-AUG-2001; 2001US-0314358P.
 XX PR 25-SEP-2001; 2001US-0325020P.
 XX PR 12-DEC-2001; 2001US-0341746P.
 XX PR 05-MAR-2002; 2002US-0362158P.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
 PI Hoersch S, Kamatkar S, Wonsley AM, Glatt K, Zhao X, Anderson D;
 XX WPI: 2003-248033/24.
 XX New nucleic acid molecule, useful for diagnosing or treating prostate
 PT cancer.
 XX Claim 1; SEQ ID NO 422; 99pp; English.
 CC The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in a
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC level indicates that the patient is afflicted with prostate cancer.
 CC Nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in

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OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 07:03:53 ; Search time 1577.61 Seconds
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Sequence: 1 gcaatcgatgggcatcctt.....ccatcaagaagattatggtt 297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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4: gb_om.*
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6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	297	100.0	297	6	A91802	A91802 Sequence 1
2	297	100.0	297	6	BD023236	BD023236 DNA for e
3	282.8	95.2	513	6	AX079459	AX079459 Sequence
C 4	282.8	95.2	635	6	AX193458	AX193458 Sequence
5	282.8	95.2	792	6	AX379319	AX379319 Sequence
6	282.8	95.2	933	6	BD070552	BD070552 Novel hum
7	282.8	95.2	1044	9	AF133425	AF133425 Homo sapi
8	282.8	95.2	1076	9	AF054838	AF054838 Homo sapi
9	282.8	95.2	1077	6	CO719831	CO719831 Sequence
10	282.8	95.2	1278	9	AF065388	AF065388 Homo sapi
11	282.8	95.2	1288	6	BD069061	BD069061 Polynucle
C 12	282.8	95.2	1288	6	BD069078	BD069078 Polynucle
13	282.8	95.2	1289	6	BD242023	BD242023 Compounds
14	282.8	95.2	1289	6	AR237206	AR237206 Sequence
15	282.8	95.2	1289	6	AR278230	AR278230 Sequence
16	282.8	95.2	1289	6	AR366926	AR366926 Sequence
17	282.8	95.2	1289	6	AR370822	AR370822 Sequence
18	282.8	95.2	1289	6	AR392327	AR392327 Sequence
19	282.8	95.2	1289	6	AR399962	AR399962 Sequence

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23	282.8	95.2	1289	6	AX106213	AX106213 Sequence
24	282.8	95.2	1289	6	AX106330	AX106330 Sequence
25	282.8	95.2	1289	6	AX140621	AX140621 Sequence
26	282.8	95.2	1289	6	AX200481	AX200481 Sequence
27	282.8	95.2	1289	6	AX267137	AX267137 Sequence
28	282.8	95.2	1289	6	BD070259	BD070259 Compounds
29	282.8	95.2	1297	9	BC007290	BC007290 Homo sapi
30	282.8	95.2	1297	9	BC013404	BC013404 Homo sapi
31	282.8	95.2	1324	6	BD195620	BD195620 70 human
32	282.8	95.2	1324	6	CQ775665	CQ775665 Sequence
33	282.8	95.2	1324	6	AR352675	AR352675 Sequence
34	282.8	95.2	1376	6	BD195552	BD195552 70 human
35	282.8	95.2	1376	6	CQ775597	CQ775597 Sequence
36	282.8	95.2	1376	6	AR352607	AR352607 Sequence
37	282.8	95.2	1533	6	BD228312	BD228312 Method of
38	282.8	95.2	1603	6	CQ414131	CQ414131 Sequence
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C 42	281.8	94.9	601	6	AX193317	AX193317 Sequence
C 43	281.8	94.9	693	6	AX193383	AX193383 Sequence
C 44	280.8	94.5	649	6	AX193358	AX193358 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS: A91802
DEFINITION: Sequence 1 from Patent WO9823775.
ACCESSION: A91802
VERSION: A91802.1 GI:6740681
KEYWORDS: unidentified
SOURCE: unidentified
ORGANISM: unclassified.
REFERENCE: 1 (bases 1 to 297)
AUTHORS: Nees,M. and Duerst,M.
TITLE: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
JOURNAL: Patent: WO 982375-A 1 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
FEATURES: Location/Qualifiers
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CDS

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 297; DB 6; Length 297;
Matches: 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAATCGATGGGGCATCTTTCTCGAAGACTTCGCGGCACCTGTCTCGTCAGTCCCATGCAG 60
Db 1 GCAATCGATGGGGCATCTTTCTCGAAGACTTCGCGGCACCTGTCTCGTCAGTCCCATGCAG 60
Qy 61 TTTTGTCAACGTGGGCTACTTCTCTCATCGACCGCGGTGTGGTCTTTGCTTTGGTTTC 120
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121 CTGGCTGCTAGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
181 CTCCTCTCATCTTCATTTGCTGAGGTTGCAGTCTGTGGTGGCTTGGTGACACCATTA 240
181 CTCCTCTCATCTTCATTTGCTGAGGTTGCAGTCTGTGGTGGCTTGGTGACACCATTA 240
241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAGATTATGTTT 297
241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAGATTATGTTT 297

RESULT 2
BD023236 297 bp DNA linear PAT 27-AUG-2002
LOCUS DNA for evaluating progress potential of cervical diseases.
DEFINITION BD023236
ACCESSION BD023236
VERSION BD023236.1 GI:22564459
KEYWORDS JP 2001504703-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 297)
AUTHORS Durust M. and Ness M.
TITLE DNA for evaluating progress potential of cervical diseases
JOURNAL Patent: JP 2001504703-A 1 10-APR-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
COMMENT PN JP 2001504703-A/1
PD 10-APR-2001
PF 12-NOV-1997 JP 1998524127
PR 27-NOV-1996 DE 19649207.6
PI MATHIAS DURUST, MATHIAS NESS
PC C12N15/09, C07K14/00, C07K16/00, C12P21/02, C12Q1/68, C12Q1/70, PC
GOIN33/574,
PC C12N15/00
CC Strandedness: Double;
CC Topology: Linear; Location/Qualifiers
FH Key Location/Qualifiers
FT CDS 1..297.
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Query Match 100.0%; Score 297; DB 6; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.2e-68;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCACTGTCTCGAGTGCCATGCAG 60
DB 1 GCAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCACTGTCTCGAGTGCCATGCAG 60
QY 61 TTGTGCAACGTGGGCTACTCTCTCATCCGACGCGGTGTGGTCTTGTCTTGGTTTC 120
DB 61 TTGTGCAACGTGGGCTACTCTCTCATCCGACGCGGTGTGGTCTTGTCTTGGTTTC 120
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RESULT 3
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Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCACTGTCTCGAGTGCCATGCAGT 61
DB 99 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCACTGTCTCGAGTGCCATGCAGT 158
QY 62 TTGTCAACGTGGGCTACTCTCTCATCCGACGCGGTGTGGTCTTGTCTTGGTTTC 121
DB 159 TTGTCAACGTGGGCTACTCTCTCATCCGACGCGGTGTGGTCTTGTCTTGGTTTC 218
QY 122 TGGCTGCTATGTTGCTAAGACTGAGACGAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 219 TGGCTGCTATGTTGCTAAGACTGAGACGAGTGTGCCCTCGTGACGTTCTTCTTCATCC 278
QY 182 TCCTCTCATCTTCATTTGCTGAGGTTGCAGTCTGTGGTGGCTTGGTGACACCATTA 241
DB 279 TCCTCTCATCTTCATTTGCTGAGGTTGCAGTCTGTGGTGGCTTGGTGACACCATTA 338
QY 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 287
DB 339 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAA 384

RESULT 4
AX193458/c
LOCUS AX193458 635 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 1025 from Patent WO0149716.
ACCESSION AX193458
VERSION AX193458.1 GI:15211409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,
Stolk, J.A., King, G.E., Wang, T., and Jiang, Y.
TITLE Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
JOURNAL Patent: WO 0149716-A 1025 12-JUL-2001;
CORIXA CORPORATION (US)
FEATURES source
1..635
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/mol_type="unassigned DNA"
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ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 635;
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Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
Db 575 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 516
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTGTGGTCTTTGCTCTTGGTTTCC 121
Db 515 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTGTGGTCTTTGCTCTTGGTTTCC 456
QY 122 TGGGCTGCTATGGTGTAAAGACTGAGCAAGTGCCTCGTGAAGTCTTCTTCATCC 181
Db 455 TGGGCTGCTATGGTGTAAAGACTGAGCAAGTGCCTCGTGAAGTCTTCTTCATCC 396
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCAGTCTGTGGTCTTGGTGTACACATAA 241
Db 395 TCCTCTCATCTTCAATGCTGAGGTTGCAGTCTGTGGTCTTGGTGTACACATAA 336
QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
Db 335 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 290

RESULT 5
AX379319
LOCUS AX379319 792 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 361 from Patent WO0196389.
ACCESSION AX379319
VERSION AX379319.1 GI:19575159
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Meagher, M.J., King, G.E., Xu, J., and Secretist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer

JOURNAL Patent: WO 0196389-A 361 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
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1. .792
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 95.2%; Score 282.8; DB 6; Length 792;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
Db 214 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 273
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTGTGGTCTTTGCTCTTGGTTTCC 121
Db 274 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTGTGGTCTTTGCTCTTGGTTTCC 333
QY 122 TGGGCTGCTATGGTGTAAAGACTGAGCAAGTGCCTCGTGAAGTCTTCTTCATCC 181
Db 334 TGGGCTGCTATGGTGTAAAGACTGAGCAAGTGCCTCGTGAAGTCTTCTTCATCC 393
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCAGTCTGTGGTGCCTTGGTGTACACATAA 241
Db 394 TCCTCTCATCTTCAATGCTGAGGTTGCAGTCTGTGGTGCCTTGGTGTACACATAA 453
QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
Db 454 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 499

RESULT 6
BD070552
LOCUS BD070552 933 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel human tumor-associated antigen.
ACCESSION BD070552
VERSION BD070552.1 GI:22616155
KEYWORDS JP 2001515349-A/1.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
AUTHORS Hillman, J.L. and Goli, S.K.
TITLE Novel human tumor-associated antigen
JOURNAL Patent: JP 2001515349-A 1 18-SEP-2001;
INCYTE PHARMACEUTICALS INC

COMMENT
OS Unidentified
PN JP 2001515349-A/1
PD 18-SEP-2001
PR 27-FEB-1998 JP 1998537919
PI JENNIFER L. HILLMAN, SURYA K. GOLI
PC CL2N15/12, C07K14/705, A61K38/12, C07K16/28, G01N33/50 CC
Strandedness: Single;
CC Topology: Linear;
CC Novel human tumor-associated antigen
FH Key Location/Qualifiers
FT source 1..933
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/organism="Unidentified".
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 95.2%; Score 282.8; DB 6; Length 933;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 61
Db 225 CAATCGATGGGCATCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT 284
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTGTGGTCTTTGCTCTTGGTTTCC 121
Db 285 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGCTGTGGTCTTTGCTCTTGGTTTCC 344
QY 122 TGGGCTGCTATGGTGTAAAGACTGAGCAAGTGCCTCGTGAAGTCTTCTTCATCC 181
Db 345 TGGGCTGCTATGGTGTAAAGACTGAGCAAGTGCCTCGTGAAGTCTTCTTCATCC 404
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCAGTCTGTGGTGCCTTGGTGTACACATAA 241
Db 405 TCCTCTCATCTTCAATGCTGAGGTTGCAGTCTGTGGTGCCTTGGTGTACACATAA 464
QY 242 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
Db 465 TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 510

RESULT 7
AF133425
LOCUS AF133425 1044 bp mRNA linear PRI 16-NOV-1999
DEFINITION Homo sapiens tetraepanin TM4-C mRNA, complete cds.
ACCESSION AF133425
VERSION AF133425.1 GI:6434903
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1044)
Puls, K.L., Ni, J., Liu, D., Morahan, G. and Wright, M.D.

Matches	284;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCGACAGTCCATGCAGT	61						
Db	98	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCGACAGTCCATGCAGT	157						
Qy	62	TTGTCAACGTGGGCTACTTCTCATCGACGCGGCGTTGTGGTCTTTGGCTCTTGGTTTCC	121						
Db	158	TTGTCAACGTGGGCTACTTCTCATCGACGCGGCGTTGTGGTCTTTGGCTCTTGGTTTCC	217						
Qy	122	TGGGCTGCTATGTTGCTTAAGACTGAGAGCAAGTGTGCCCTCGTACGCTTCTTTCATCC	181						
Db	218	TGGGCTGCTATGTTGCTTAAGACTGAGAGCAAGTGTGCCCTCGTACGCTTCTTTCATCC	277						
Qy	182	TCCTCCTCATCTTTCATGTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGACACCAATAA	241						
Db	278	TCCTCCTCATCTTTCATGTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGACACCAATAA	337						
Qy	242	TGCGTGAGCACTTCCCGACGTTCTGTAGTGCCTGCCATCAAGAA	287						
Db	338	TGCGTGAGCACTTCCCGACGTTCTGTAGTGCCTGCCATCAAGAA	383						
RESULT	10								
LOCUS	AF065388								
DEFINITION	Homo sapiens tetraspan NET-1 mRNA, complete cds.								
ACCESSION	AF065388								
VERSION	AF065388.1	GI:3152700							
KEYWORDS	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
TITLE	1 (bases 1 to 1278)								
JOURNAL	Serru,V., Bessen,P., Boucheix,C. and Rubinstein,E.								
MEDLINE	Sequence and expression of seven new tetraspans								
PUBMED	Biochim. Biophys. Acta 1478 (1), 159-163 (2000)								
REFERENCE	10719184								
AUTHORS	2 (bases 1 to 1278)								
TITLE	Rubinstein,E., Serru,V. and Boucheix,C.								
JOURNAL	Direct Submission								
FEATURES	Submitted (14-MAY-1998) INSERM U268, 14 av Paul Vaillant Couturier, Villejuif 94807, France								
source	Location/Qualifiers								
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	/clone="IMAGE ID 511239"								
	122..847								
	/note="similar to Tspan-1; TM4SF"								
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	/product="tetraspan NET-1"								
	/protein_id="AAC17119.1"								
	/db_xref="GI:3152701"								
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	SPVFKENSAFPPECCNDVNTANETCTKQKAHDQKVEGCFNQLLYDIRTNAVTVGGV								
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ORIGIN									
Query Match	95.2%	Score 282.8;	DB 9;	Length 1278;					
Best Local Similarity	99.3%;	Pred. No. 1.4e-64;							
Matches 284; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;					
Qy	2	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCGACAGTCCATGCAGT	61						
Db	219	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCGACAGTCCATGCAGT	278						
Qy	62	TTGTCAACGTGGGCTACTTCTCATCGACGCGGCGTTGTGGTCTTTGGCTCTTGGTTTCC	121						

QY 242 TGGCTGAGCAGCTTCCGAGTTCCTGCTGCTAGTCCCTGCCATCAAGAA 287
|||||
Db 455 TGGCTGAGCAGCTTCTGAGCTTGGTGGTAGTGCCTGCCATCAAGAA 500
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RESULT 12

BD069078/c
LOCUS BD069078 1288 bp DNA linear PAT 27-AUG-2002
DEFINITION Polynucleotides and polypeptides encoding receptors.
ACCESSION BD069078
KEYWORDS JP 2001509679-A/21.
SOURCE unclassified
ORGANISM unclassified

REFERENCE

1 (bases 1 to 1288)
AUTHORS Ni,J., Gentz,R.L. and Rosen,C.A.
TITLE Polynucleotides and polypeptides encoding receptors
JOURNAL Patent: JP 2001509679-A 21 24-JUL-2001;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2001509679-A/21
PD 24-JUL-2001
PF 21-JAN-1998 JP 1998534602
PR 21-JAN-1997 US 60/034204,21-JAN-1997 US 60/034205 PI
JIAN NI,REINER L GENTZ,CRAIG A ROSEN
PC C12N15/12,C12N15/85,C12N5/10,C07K14/705,C07K16/28,C12Q1/68, PC
A61K38/17,
PC A61K48/00
CC Strandedness: Single;
CC Topology: Linear;
CC Polynucleotides and polypeptides encoding receptors FH Key
Location/Qualifiers
FT source 1..1288
FT /organism='Unidentified'.

FEATURES

source
1..1288
/organism="unidentified"
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/db_xref="taxon:32644"

ORIGIN

Query Match 95.2%; Score 282.8; DB 6; Length 1288;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
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Db 1074 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 1015
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QY 62 TTGTCAAGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTGTCTTTGGTTTCC 121
|||||

Db 1014 TTGTCAAGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTGTCTTTGGTTTCC 955
|||||

QY 122 TGGGCTGCTATCGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGCAGTTCCTTCATCC 181
|||||

Db 954 TGGGCTGCTATCGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGCAGTTCCTTCATCC 895
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QY 182 TCCTCCTCATCTTCATGCTGAGTTGAGTGTGCTGTGGTGCCTTGGTGACACATAA 241
|||||

Db 894 TCCTCCTCATCTTCATGCTGAGTTGAGTGTGCTGTGGTGCCTTGGTGACACATAA 835
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QY 242 TGGCTGAGCAGCTTCCGAGTTCCTGCTAGTTCCTGCCATCAAGAA 287
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Db 834 TGGCTGAGCAGCTTCTGAGCTTGGTAGTGCCTGCCATCAAGAA 789
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RESULT 13

BD242023
LOCUS BD242023 1289 bp DNA linear PAT 17-JUL-2003
DEFINITION Compounds for immunotherapy and diagnosis of prostate cancer and
methods for their use.
ACCESSION BD242023

VERSION BD242023.1 GI:33051793

KEYWORDS JP 2002520054-A/110.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1289)

Dillon,D.C., Harlocker,S.L., Yudi,J., Xu,J. and Mitcham,J.L.

Compounds for immunotherapy and diagnosis of prostate cancer and

methods for their use

Patent: JP 2002520054-A 110 09-JUL-2002;

CORIXA CORP

OS Homo sapiens (human)

PN JP 2002520054-A/110

PD 09-JUL-2002

PF 14-JUL-1999 JP 2000560247

PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR

23-SEP-1998 US 09/159822,23-SEP-1998 US 09/159812 PR

15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR

09-APR-1999 US 09/288946

PI DAVIN CLIFFORD DILLON,SUSAN LOUISE HARLOCKER,JIANG YUQIU, PI

JIANGCHUN XU,

PI JENNIFER LYNN MITCHAM

PC C12N15/09,A61K38/00,A61K39/395,C07K14/47,C07K16/30,

PC C12N5/10,

PC C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,

PC A61K37/02,

PC C12N5/00

CC Compounds for immunotherapy and diagnosis of prostate cancer

and methods

CC for their use

FH Key Location/Qualifiers

FT source 1..1289

/organism='Homo sapiens (human)'.

Location/Qualifiers

1..1289

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

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Query Match 95.2%; Score 282.8; DB 6; Length 1289;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
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Db 220 CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 279
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QY 62 TTGTCAAGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTCC 121
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Db 280 TTGTCAAGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGGTTTCC 339
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QY 122 TGGGCTGCTATGCTAAGACTGAGAGCAAGTGTGCCCTCGTGCAGTTCCTTCATCC 181
|||||

Db 340 TGGGCTGCTATGCTAAGACTGAGAGCAAGTGTGCCCTCGTGCAGTTCCTTCATCC 399
|||||

QY 182 TCCTCCTCATCTTCATGCTGAGTTGAGTGTGCTGTGGTGCCTTGGTGACACATAA 241
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Db 400 TCCTCCTCATCTTCATGCTGAGTTGAGTGTGCTGTGGTGCCTTGGTGACACATAA 459
|||||

QY 242 TGGCTGAGCAGCTTCCGAGTTCCTGCTAGTTCCTGCCATCAAGAA 287
|||||

Db 460 TGGCTGAGCAGCTTCTGACGTTGCTGCTAGTTCCTGCCATCAAGAA 505
|||||

RESULT 14

AR237206
LOCUS AR237206 1289 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 111 from patent US 6465611.
ACCESSION AR237206
VERSION AR237206.1 GI:27281864
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1289)
AUTHORS Xu,J., Dillon,D.C. and Mitcham,J.L.
TITLE Compounds for immunotherapy of prostate cancer and methods for their use
JOURNAL Patent: US 6465611-A 111 15-OCT-2002;
FEATURES Location/Qualifiers
 1..1289
 /organism="unknown"
 /mol_type="genomic DNA"
ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 1289;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 61
DB 220 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGAGCCGGCGTGTGGTCTTTGGTTTCC 121
DB 280 TTGTCAACGTGGGCTACTTCTCATCGAGCCGGCGTGTGGTCTTTGGTTTCC 339
QY 122 TGGGCTGCTATGCTGTAGACTTGAGCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 181
DB 340 TGGGCTGCTATGCTGTAGACTTGAGCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 399
QY 182 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTTCGCTTGGTGTACACCAATAA 241
DB 400 TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTTCGCTTGGTGTACACCAATAA 459
QY 242 TGGCTGAGCACTTCCGACGTTGCTGCTAGTGCCTCGTGAGCTTCTTTCATCAAGAA 287
DB 460 TGGCTGAGCACTTCCGACGTTGCTGCTAGTGCCTCGTGAGCTTCTTTCATCAAGAA 505

RESULT 15
AR278230
LOCUS AR278230 1289 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 111 from patent US 6512094.
ACCESSION AR278230
VERSION AR278230.1 GI:29712476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1289)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedwick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hedler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6512094-A 111 28-JAN-2003;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 1289;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 61
DB 220 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCACAGTGCATGCAGT 279
QY 62 TTGTCAACGTGGGCTACTTCTCATCGAGCCGGCGTGTGGTCTTTGGTTTCC 121

Search completed: August 27, 2005, 09:49:23
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GenCore version 5.1.1.6
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Title: US-10-079-954-1

Perfect score: 297

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283.2	95.4	777	7	CF595432
2	282.8	95.2	518	6	CB161656 K-EST0221
3	282.8	95.2	539	6	CD709223 EST25750
4	282.8	95.2	542	4	BM819747
5	282.8	95.2	543	4	BM819711
6	282.8	95.2	546	6	CD700012 EST16536
7	282.8	95.2	549	2	BE249898 600942941
8	282.8	95.2	554	4	BM819756 K-EST0087
9	282.8	95.2	559	5	EX480177 DKFZp686E
10	282.8	95.2	564	4	BG428609 602494743
11	282.8	95.2	566	4	BM819724 K-EST0087
12	282.8	95.2	568	5	BP261193 BP261193
13	282.8	95.2	568	5	BP262643 BP262643
14	282.8	95.2	571	4	BM819701
15	282.8	95.2	571	5	BP262874
16	282.8	95.2	573	5	BP263326
17	282.8	95.2	576	5	BP260827
18	282.8	95.2	579	6	CD701289
19	282.8	95.2	581	5	BP254783
20	282.8	95.2	581	5	BP262395
21	282.8	95.2	582	5	BP260782
22	282.8	95.2	582	5	BP261111
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24	282.8	95.2	582	5	BP263741

25	282.8	95.2	582	5	BP276804	BP276804
26	282.8	95.2	582	5	BP330600	BP330600
27	282.8	95.2	582	5	BP330653	BP330653
28	282.8	95.2	582	5	BP330738	BP330738
29	282.8	95.2	582	5	BP330807	BP330807
30	282.8	95.2	582	6	CD698393	CD698393
31	282.8	95.2	583	4	BM819683	BM819683
32	282.8	95.2	583	5	BP255135	BP255135
33	282.8	95.2	583	5	BP260638	BP260638
34	282.8	95.2	583	5	BP262132	BP262132
35	282.8	95.2	583	5	BP342136	BP342136
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37	282.8	95.2	585	5	BP331321	BP331321
38	282.8	95.2	585	6	CB216655	CB216655
39	282.8	95.2	586	4	BM836692	BM836692
40	282.8	95.2	601	4	BM819685	BM819685
41	282.8	95.2	604	6	CD704563	CD704563
42	282.8	95.2	610	6	CD699899	CD699899
43	282.8	95.2	613	4	BM828457	BM828457
44	282.8	95.2	614	6	CD691226	CD691226
45	282.8	95.2	622	6	CD698114	CD698114

ALIGNMENTS

RESULT 1
CF595432
LOCUS
DEFINITION
CF595432
IMAGE:30703089 5', mRNA sequence.
ACCESSION
CF595432.1 GI:36350884
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 777)
NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Arnold Schwartz, MD, PhD
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDCM249. row: p column: 10
High quality sequence stop: 453.
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Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="Stomach, adenocarcinoma"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI CGAP St"

by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).¹⁸

ORIGIN	Query Match	95.4%	Score 283.2	DB 7	Length 777
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Db	241	CAATCGAATGGGCAATCCTTCTGAAGATCTTTCGGGCCACTGTCGTCAGTGCCATGCAAGT	300		
Qy	62	TTGTCAACGTTGGGCTACTTTCCTCATCGCAGCGCGGTTGTGGTCTTTGGTCTTTGGTTTCC	121		
Db	301	TTGTCAACGTTGGGCTACTTTCCTCATCGCAGCGCGGTTGTGGTCTTTGGTCTTTGGTTTCC	360		
Qy	122	TGGGCTGCTATGGTGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTTCATCC	181		
Db	361	TGGGCTGCTATGGTGTCTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTTCATCC	420		
Qy	182	TCCTTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGTGGTCGCCTTGGTGACCAATAA	241		
Db	421	TCCTTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGTGGTCGCCTTGGTGACCAATAA	480		
Qy	242	TGGCTGAGCACTTCGCGACGTTGCTGGTAGTGCCTTGCCATCAAGAAGA	289		
Db	481	TGGCTGAGCACTTCGCGACGTTGCTGGTAGTGCCTTGCCATCAAGAATAA	528		

RESULT 2	518 bp	linear	EST 30-JAN-2003
CB161656			
LOCUS	K-EST0221639	L18POOL1n1	Homo sapiens cDNA clone L18POOL1n1-48-D07
DEFINITION	5', mRNA sequence.		
ACCESSION	CB161656		
VERSION	CB161656.1	GI:28147782	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 518)		
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.		
TITLE	21C Frontier Korean EST Project 2001		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: kim ys		

ORIGIN

	Query Match	95.2%	Score 282.8;	DB 6;	Length 539;
	Best Local Similarity	99.3%;	Pred. No. 3.1e-68;		
	Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	2	CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTCGCATGCAGT	61		
Db	156	CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTCGCATGCAGT	215		
Qy	62	TTTGTCACGTGGGCTACTTCCTCATCGCAGCGCGTTGTGGTCTTGTCTCTGGTTTCC	121		
Db	216	TTTGTCACGTGGGCTACTTCCTCATCGCAGCGCGTTGTGGTCTTGTCTCTGGTTTCC	275		
Qy	122	TGGGCTGCTATGGTGCCTAAAGACTGAGAGCAAGTGTGCCCTCGTGACGCTCTTCTTCATCC	181		

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Db      276  TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTCTTCTTCATCC 335
      |||
Qy      182  TCTCTCCTCATCTTCATCTGCTGAGGTGCGAGCTGCTGTGCTGCGCTGGTGTACACATAA 241
      |||
Db      336  TCTCTCCTCATCTTCATCTGCTGAGGTGCGAGCTGCTGTGCTGCGCTGGTGTACACACAA 395
      |||
Qy      242  TGGCTGAGCACTTCCCGAGCTTGTCTGCTAGTGTGCTGCCATCAAGAA 287
      |||
Db      396  TGGCTGAGCACTTCTGAGCTTGTCTGCTAGTGTGCTGCCATCAAGAA 441
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RESULT 4
BM819747
LOCUS    K-EST0087909 S18N669761 Homo sapiens cDNA clone S18N669761-20-G10
DEFINITION 5', mRNA sequence.
ACCESSION BM819747
VERSION   BM819747.1 GI:19176160
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
           Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
           Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
           Genome Research Center
           Korea Research Institute of Bioscience & Biotechnology
           52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
           Tel: +82-42-860-4470
           Fax: +82-42-860-4409
           Email: yongsung@mail.kribb.re.kr
           Plate: 20 row: G column: 10
           High quality sequence stop: 542.
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               /clone="S18N669761-20-G10"
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               /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
               Site 2: NotI; The poly (A) + RNA was dephosphorylated with
               bacterial alkaline phosphatase (BAP) and then decapped
               with tobacco acid pyrophosphatase (TAP). The decapped
               intact mRNA was ligated with DNA-RNA linker including EcoR
               I site by treatment of T4 RNA ligase and the first strand
               cDNA was synthesized from oligo dT-selected mRNA by
               priming with dT-tailed vector. The dT-tailed vector was
               adjusted to have about 60nt. The cDNA vector was
               circularized with E. coli DNA ligase after digestion of
               EcoRI which site is also included in vector. An RNA strand
               converted to a DNA strand by Okayama-Berg method. The
               obtained cDNA vectors were used for transfection of
               competent cells E. coli Top10F, by electroporation method.
               The cDNA libraries constructed by this method are
               full-length enriched cDNA library."

ORIGIN
Query Match 95.2%; Score 282.8; DB 4; Length 542;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CAATCGATGGGCGATCTTTTCTGAAGATCTTCGGGCCACTGTCGTCACAGTGCCATGCAGT 61
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Qy      62  TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTTCC 121
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Qy      122  TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTCTTCTTCATCC 181
      |||
Db      326  TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTCTTCTTCATCC 385
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Qy      182  TCCTCCTCATCTTCATCTGCTGAGGTGCGAGCTGCTGTGCTGCCCTGGTGTACACATAA 241
      |||
Db      386  TCCTCCTCATCTTCATCTGCTGAGGTGCGAGCTGCTGTGCTGCCCTGGTGTACACACAA 445
      |||

Qy      242  TGGCTGAGCACTTCCCGAGCTTGTCTGCTAGTGTGCTGCCATCAAGAA 287
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Db      446  TGGCTGAGCACTTCTGAGCTTGTCTGCTAGTGTGCTGCCATCAAGAA 491
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RESULT 5
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LOCUS    K-EST0087869 S18N669761 Homo sapiens cDNA clone S18N669761-20-D06
DEFINITION 5', mRNA sequence.
ACCESSION BM819711
VERSION   BM819711.1 GI:19176124
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
           Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
           Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
           Genome Research Center
           Korea Research Institute of Bioscience & Biotechnology
           52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
           Tel: +82-42-860-4470
           Fax: +82-42-860-4409
           Email: yongsung@mail.kribb.re.kr
           Plate: 20 row: D column: 06
           High quality sequence stop: 543.
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               /clone="S18N669761-20-D06"
               /sex="F"
               /lab_host="Top10F"
               /clone_lib="S18N669761"
               /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
               Site 2: NotI; The poly (A) + RNA was dephosphorylated with
               bacterial alkaline phosphatase (BAP) and then decapped
               with tobacco acid pyrophosphatase (TAP). The decapped
               intact mRNA was ligated with DNA-RNA linker including EcoR
               I site by treatment of T4 RNA ligase and the first strand
               cDNA was synthesized from oligo dT-selected mRNA by
               priming with dT-tailed vector. The dT-tailed vector was
               adjusted to have about 60nt. The cDNA vector was
               circularized with E. coli DNA ligase after digestion of
               EcoRI which site is also included in vector. An RNA strand
               converted to a DNA strand by Okayama-Berg method. The
               obtained cDNA vectors were used for transfection of
               competent cells E. coli Top10F, by electroporation method.
               The cDNA libraries constructed by this method are
               full-length enriched cDNA library."

ORIGIN
Query Match 95.2%; Score 282.8; DB 4; Length 543;

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Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db |||
QY 246 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 305
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QY 62 TTGTCAACGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGCTTTCC 121
Db |||
QY 306 TTGTCAACGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGCTTTCC 365
Db |||
QY 122 TGGGCTGCTATGCTGAAGACTGAGACCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 181
Db |||
QY 366 TGGGCTGCTATGCTGAAGACTGAGACCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 425
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QY 182 TCCTCCTCATCTTCAATGCTGAGTGTGACGCTGCTGTGGTGCCTTGTGTACACATAA 241
Db |||
QY 426 TCCTCCTCATCTTCAATGCTGAGTGTGACGCTGCTGTGGTGCCTTGTGTACACATAA 485
Db |||
QY 242 TGGGCTGAGCACTTCGCGAGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db |||
QY 486 TGGGCTGAGCACTTCGCGAGTTGCTGTAGTGCCTGCCATCAAGAA 531
Db |||

RESULT 6
LOCUS CD700012 546 bp mRNA linear EST 25-JUN-2003
DEFINITION EST16536 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD700012
VERSION CD700012.1 GI:32229841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsuums.edu.cn.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN
Query Match 95.2%; Score 282.8; DB 6; Length 546;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
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QY 255 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 314
Db |||
QY 62 TTGTCAACGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGCTTTCC 121
Db |||
QY 315 TTGTCAACGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGCTTTCC 374
Db |||
QY 122 TGGGCTGCTATGCTGAAGACTGAGACCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 181
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QY 375 TGGGCTGCTATGCTGAAGACTGAGACCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 434
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QY 182 TCCTCCTCATCTTCAATGCTGAGTGTGACGCTGCTGTGGTGCCTGCCATCAAGAA 241
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QY 242 TGGGCTGAGCACTTCGCGAGTTGCTGTAGTGCCTGCCATCAAGAA 287
Db |||
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Db |||

RESULT 7
LOCUS BE249898 549 bp mRNA linear EST 13-JUL-2000
DEFINITION 60942941P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959379 5',
mRNA sequence.
ACCESSION BE249898
VERSION BE249898.1 GI:9120001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 549)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LiCM51 row: a column: 12
High quality sequence stop: 549.
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adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN
Query Match 95.2%; Score 282.8; DB 2; Length 549;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db |||
QY 206 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 265
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QY 62 TTGTCAACGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGCTTTCC 121
Db |||
QY 266 TTGTCAACGTGGGCTACTTCCTCATCGCAGCGGGTGTGGTCTTTGCTCTTGCTTTCC 325
Db |||
QY 122 TGGGCTGCTATGCTGAAGACTGAGACCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 181
Db |||
QY 326 TGGGCTGCTATGCTGAAGACTGAGACCAAGTGTGCCCTCGTGAGCTTCTTTCATCC 385
Db |||
QY 182 TCCTCCTCATCTTCAATGCTGAGTGTGACGCTGCTGTGGTGCCTGCCATCAAGAA 241
Db |||
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Db 386 TCCTCCTCATCTTCATTGCTGAGAGTTCGACGCTGCTGTGGTGCCTTGGTGATACCAACAA 445
 Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAA 287
 Db 446 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCGCATCAAGAA 491

RESULT 8
 BM819756 554 bp mRNA linear EST 06-MAR-2002
 LOCUS K-EST0087919 S18N669761 Homo sapiens cDNA clone S18N669761-20-H08
 DEFINITION 5', mRNA sequence.
 ACCESSION BM819756
 VERSION BM819756.1 GI:19176169
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 554)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.kribb.re.kr
 Plate: 20 row: H column: 08
 High quality sequence stop: 554.

FEATURES
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 /clone_lib="S18N669761"
 /notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoRI
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN
 Query Match 95.2%; Score 282.8; DB 4; Length 554;
 Best Local Similarity 99.3%; Pred. No. 3.1e-68;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCGTCCAGTGCCATGCAGT 61
 Db 231 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGCGTCCAGTGCCATGCAGT 290
 Qy 62 TTGTCAACGTGGGCTACTTCTCATCCGACCGCGGTGTGGTCTTGTGCTCTGGTTTCC 121
 Db 291 TTGTCAACGTGGGCTACTTCTCATCCGACCGCGGTGTGGTCTTGTGCTCTGGTTTCC 350

Db 414 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGCTGCTTGGTGATACACCACA 473
 QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGGCTTGCCTGCATCAAGAA 287
 Db 474 TGGCTGAGCACTTCCCTGACGTTGCTGTAGTGGCTTGCCTGCATCAAGAA 519

RESULT 10
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 DEFINITION 602494743F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608394 5', mRNA sequence.
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 VERSION BG428609.1 GI:13335115
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLM1350 row: f column: 11
 High quality sequence stop: 560.

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 /clone_lib="NIH MGC_75"
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccggccg); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

ORIGIN
 Query Match 95.2%; Score 282.8; DB 4; Length 564;
 Best Local Similarity 99.3%; Pred. No. 3.1e-68;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
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 QY 122 TGGGCTGTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTAGAGTTCTTCTTCATCC 181
 Db 353 TGGGCTGTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTAGAGTTCTTCTTCATCC 412
 QY 182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGATACACCAPAA 241

Db 413 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGCTGCTTGGTGATACACCACA 472
 QY 242 TGGCTGAGCACTTCCGACGTTGCTGTAGTGGCTTGCCTGCATCAAGAA 287
 Db 473 TGGCTGAGCACTTCCCTGACGTTGCTGTAGTGGCTTGCCTGCATCAAGAA 518

RESULT 11
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 ACCESSION BM819724
 VERSION BM819724.1 GI:19176137
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 566)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: vongeeung@mail.kribb.re.kr
 Plate: 20 row: E column: 08
 High quality sequence stop: 566.
 Location/Qualifiers

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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S18N669761-20-E08"
 /sex="F"
 /lab_host="Top10P"
 /clone_lib="S18N669761"
 /note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 50nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN
 Query Match 95.2%; Score 282.8; DB 4; Length 566;
 Best Local Similarity 99.3%; Pred. No. 3.1e-68;
 Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCATGCAGT 61
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 QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCCGGGTGTGGTCTTTGCTCTTGGTTTCC 121
 Db 292 TTGTCAACGTGGGCTACTTCTCATCGACGCCGGGTGTGGTCTTTGCTCTTGGTTTCC 351


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Qy 122 TGCGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTGTCAGCGTTCTTCTTCATCC 181
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Qy 182 TCCTCCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGACACCAATAA 241
Db 412 TCCTCCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGACACCAAA 471
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGGCCATCAAGAA 287
Db 472 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGGCCATCAAGAA 517

RESULT 12
BP261193 568 bp mRNA linear EST 16-SEP-2004
LOCUS BP261193 Sugano cDNA library, small intestine Homo sapiens CDNA
DEFINITION clone HSI02743, mRNA sequence.
ACCESSION BP261193
VERSION BP261193.1 GI:52176424
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 568)
AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
FEATURES
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Db 238 CATTGATGGGCATCCTTTCTGAGATCTTCGGGCCACTGTGTCAGTGCATGCAGT 297
Qy 62 TTGTCAAGTGGGCTACTTCCTCATCGACCGCGGTTGTGGTCTTTGGCTTTGGTTTC 121
Db 298 TTGTCAAGTGGGCTACTTCCTCATCGACCGCGGTTGTGGTCTTTGGCTTTGGTTTC 357
Qy 122 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTGTCGAGCGTTCTTCTTCATCC 181
Db 358 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTGTCGAGCGTTCTTCTTCATCC 417
Qy 182 TCCTCCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGACACCAATAA 241
Db 418 TCCTCCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGACACCAAA 477
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RESULT 13
BP262643

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ACCESSION	BP262643											
VERSION	BP262643.1	GI:52177874										
KEYWORDS	EST.											
SOURCE	Homo sapiens (human)											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
AUTHORS	1 (bases 1 to 568)											
TITLE	Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.											
JOURNAL	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions											
COMMENT	Genome Res. 14 (9), 1711-1718 (2004)											
FEATURES	Contact: Yutaka Suzuki											
source	Department of Virology											
	Institute of Medical Science, University of Tokyo											
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan											
	Email: yusuzuki@ims.u-tokyo.ac.jp.											
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Qy	62	TTGTCAACGTGGGCTACTTCTCATCGACGCGCGTGTGGCTTTGCTTGGTTTCC	121									
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Qy	122	TGGGCTGCTATGTGTCTAAGACCTGAGACGAAGTGTGCCCTCGTGCAGCTTCTTCTTCATCC	181									
Db	353	TGGGCTGCTATGTGTCTAAGACCTGAGACGAAGTGTGCCCTCGTGCAGCTTCTTCTTCATCC	412									
Qy	182	TCCTCTCATCTTCATGTCGAGTTGCGAGTCTCTGTGGCTGGTGTCACCATAA	241									
Db	413	TCCTCTCATCTTCATGTCGAGTTGCGAGTCTCTGTGGCTGGTGTCACCATAA	472									
Qy	242	TGGCTGAGCAGTCCCGAGTGTCTGTAGTGCCTGCCATCAGAA	287									
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ORGANISM	Homo sapiens											
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AUTHORS	1 (bases 1 to 571)											
	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.											
TITLE	21C Frontier Korean EST Project 2001											

JOURNAL
COMMENT

Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: C column: 03
High quality sequence stop: 571.
Location/Qualifiers
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/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

FEATURES
source

1. 571
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/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 95.2%; Score 282.8; DB 4; Length 571;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
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QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTCTTGGTTTCC 121
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DB 357 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 416
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DB 417 TCCTCTCATCTTCAATTCGTAGAGTTCAGAGTGCCTCGTGCAGTTCCTTCTTCATCC 476
QY 242 TGGCTGAGCATTCCCGACGTTGCTGTTAGTGCCTGCCATCAAGAA 287
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RESULT 15
BP262874

LOCUS BP262874 Sugano cDNA library, 571 bp mRNA linear EST 16-SEP-2004
DEFINITION clone HS108372, mRNA sequence.
ACCESSION BP262874
VERSION BP262874.1 GI:52178105
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 571)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL

Contact: Yutaka Suzuki
Department of Virology

COMMENT

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1. 571
/organism="Homo sapiens"
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ORIGIN

Query Match 95.2%; Score 282.8; DB 5; Length 571;
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
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QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 233 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 292
QY 62 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTCTTGGTTTCC 121
DB 293 TTGTCAACGTGGGCTACTTCTCATCGACGCGGGCTTGCTGCTCTTTGCTCTTGGTTTCC 352
QY 122 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 181
DB 353 TGGGCTGCTATGCTGTAGAGCTGAGAGCAAGTGCCTCGTGCAGTTCCTTCTTCATCC 412
QY 182 TCCTCTCATCTTCAATTCGTAGAGTTCAGAGTGCCTCGTGCAGTTCCTTCTTCATCC 241
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QY 242 TGGCTGAGCATTCCCGACGTTGCTGTTAGTGCCTGCCATCAAGAA 287
DB 473 TGGCTGAGCATTCCCTGAGCTTGCTGTTAGTGCCTGCCATCAAGAA 518

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: August 27, 2005, 08:38:03 ; Search time 545.032 Seconds
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Scoring table: IDENTITY NUC
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Searched: 7331713 seqs, 3271544945 residues
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	282.8	95.2	635	9	Sequence 203, App
c	282.8	95.2	635	9	Sequence 1025, Ap
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c	282.8	95.2	635	13	Sequence 1025, Ap
6	282.8	95.2	792	9	Sequence 361, App
7	282.8	95.2	1044	19	Sequence 132, App

8	282.8	95.2	1076	14	US-10-097-340-325	Sequence 325, App
9	282.8	95.2	1076	15	US-10-205-823-424	Sequence 424, App
10	282.8	95.2	1076	17	US-10-172-118-1191	Sequence 1191, App
11	282.8	95.2	1076	18	US-10-342-887-1191	Sequence 1191, App
12	282.8	95.2	1076	19	US-10-775-920-136	Sequence 136, App
13	282.8	95.2	1154	14	US-10-097-340-323	Sequence 323, App
14	282.8	95.2	1154	15	US-10-205-823-422	Sequence 422, App
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17	282.8	95.2	1278	19	US-10-775-920-130	Sequence 130, App
18	282.8	95.2	1288	15	US-10-156-136-4	Sequence 4, Appli
19	282.8	95.2	1288	15	US-10-156-136-50	Sequence 50, Appli
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28	282.8	95.2	1289	9	US-09-895-793-111	Sequence 111, App
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30	282.8	95.2	1289	13	US-10-012-896-111	Sequence 111, App
31	282.8	95.2	1289	14	US-10-010-940-111	Sequence 111, App
32	282.8	95.2	1289	16	US-10-144-678A-111	Sequence 111, App
33	282.8	95.2	1289	16	US-10-294-025-111	Sequence 111, App
34	282.8	95.2	1289	19	US-10-688-838-111	Sequence 111, App
35	282.8	95.2	1297	19	US-10-775-920-131	Sequence 131, App
36	282.8	95.2	1297	19	US-10-775-920-133	Sequence 133, App
37	282.8	95.2	1306	19	US-10-775-920-134	Sequence 134, App
38	282.8	95.2	1324	9	US-09-981-876-82	Sequence 82, Appl
39	282.8	95.2	1324	10	US-09-148-545-82	Sequence 82, Appl
40	282.8	95.2	1376	9	US-09-981-876-14	Sequence 14, Appl
41	282.8	95.2	1376	10	US-09-148-545-14	Sequence 14, Appl
42	282.8	95.2	1456	9	US-09-981-353-133	Sequence 133, App
43	282.8	95.2	1533	21	US-10-918-897-14	Sequence 14, Appl
44	282.8	95.2	1603	10	US-09-814-353-21202	Sequence 21202, A
45	282.8	95.2	1603	20	US-10-357-930-23347	Sequence 23347, A

ALIGNMENTS

RESULT 1

US-10-079-954-1

; Sequence 1, Application US/10079954

; Publication No. US2002016861A1

; GENERAL INFORMATION:

; APPLICANT: Nees, Matthias

; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS

; FILE REFERENCE: SCHU 204 (09302857)

; CURRENT APPLICATION NUMBER: US/10/079,954

; CURRENT FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: US/09/308,984

; PRIOR FILING DATE: 1999-09-03

; PRIOR APPLICATION NUMBER: PCT/DE97/02660

; PRIOR FILING DATE: 1996-11-12

; PRIOR APPLICATION NUMBER: DE 196 49207

; PRIOR FILING DATE: 1997-11-27

; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 1

; LENGTH: 297

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-079-954-1

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Best Local Similarity 100.0%; Pred. No. 1.3e-84;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; OTHER INFORMATION: n = A,T,C or G
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Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTTGTGTCCTTTGCTCTTGGTTTCC 121
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QY 182 TCCTCCTCATCTTCATTCCTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGTACACCAAA 241
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RESULT 6
US-09-878-134-361
; Sequence 361, Application US/09878134
; Publication No. US20020086303A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.532
; CURRENT APPLICATION NUMBER: US/09/878,134
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 361
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-878-134-361

Query Match          95.2%; Score 282.8; DB 9; Length 792;
Best Local Similarity 99.3%; Pred. No. 5.8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db 214 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 273
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTTGTGTCCTTTGCTCTTGGTTTCC 121
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QY 122 TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGCCTCGTGACGTTCTTCTTCATCC 181
Db 334 TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGCCTCGTGACGTTCTTCTTCATCC 393
QY 182 TCCTCCTCATCTTCATTCCTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGTACACCAAA 241
Db 394 TCCTCCTCATCTTCATTCCTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGTACACCAAA 453
QY 242 TGGCTGAGCACTTCCGAGGTTGCTGGTAGTGCTTGCCTGCCATCAAGAA 287
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; Sequence 132, Application US/10775920
; Publication No. US2004017544A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1025
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; TYPE: DNA
; ORGANISM: Homo sapiens
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; LOCATION: 618
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1025

Query Match          95.2%; Score 282.8; DB 13; Length 635;
Best Local Similarity 99.3%; Pred. No. 5.4e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
Db 575 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 516
QY 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTTGTGTCCTTTGCTCTTGGTTTCC 121
Db 515 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTTGTGTCCTTTGCTCTTGGTTTCC 456
QY 122 TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGCCTCGTGACGTTCTTCTTCATCC 181
Db 455 TGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGCCTCGTGACGTTCTTCTTCATCC 396
QY 182 TCCTCCTCATCTTCATTCCTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGTACACCAAA 241
Db 395 TCCTCCTCATCTTCATTCCTGAGGTTGCAGCTGCTGTGTGTCGCTTGGTGTACACCAAA 336
QY 242 TGGCTGAGCACTTCCGAGGTTGCTGGTAGTGCTTGCCTGCCATCAAGAA 287
Db 335 TGGCTGAGCACTTCCGAGGTTGCTGGTAGTGCTTGCCTGCCATCAAGAA 290

RESULT 5
US-10-025-380-1025/c
; Sequence 1025, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clepper, Jonathan D.
; APPLICANT: Skeiky, Yashir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 618
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1025
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; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-132

Query Match          95.2%; Score 282.8; DB 19; Length 1044;
Best Local Similarity 99.3%; Pred. No. 6.2e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 221 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 280
QY 62 TTGTCAAGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTTTCC 121
DB 281 TTGTCAAGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTTTCC 340
QY 122 TGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGTTCCTTCTTCATCC 181
DB 341 TGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAGTTCCTTCTTCATCC 400
QY 182 TCCTCCTCATCTTCACTTGCTGAGGTTGACGCTGCTGTGGTGCCTTGGTGACACCAAA 241
DB 401 TCCTCCTCATCTTCACTTGCTGAGGTTGACGCTGCTGTGGTGCCTTGGTGACACCAAA 460
QY 242 TGGCTGAGCAGTTCCTCCGAGTTGCTGCTAGTGCCTGCGCCATCAAGAA 287
DB 461 TGGCTGAGCAGTTCCTGAGTTGCTGCTAGTGCCTGCGCCATCAAGAA 506

RESULT 8
US-10-097-340-325
; Sequence 325, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Katen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
```

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; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-325

Query Match          95.2%; Score 282.8; DB 14; Length 1076;
Best Local Similarity 99.3%; Pred. No. 6.3e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 61
DB 98 CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCCATGCAGT 157
QY 62 TTGTCAAGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTTTCC 121
DB 158 TTGTCAAGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTTTCC 217
QY 122 TGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
QY 182 TCCTCCTCATCTTCACTTGCTGAGGTTGACGCTGCTGTGGTGCCTTGGTGACACCAAA 241
DB 278 TCCTCCTCATCTTCACTTGCTGAGGTTGACGCTGCTGTGGTGCCTTGGTGACACCAAA 337
QY 242 TGGCTGAGCAGTTCCTCCGAGTTGCTGCTAGTGCCTGCGCCATCAAGAA 287
DB 338 TGGCTGAGCAGTTCCTGAGTTGCTGCTAGTGCCTGCGCCATCAAGAA 383

RESULT 9
US-10-205-823-424
; Sequence 424, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoerschi, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
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; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED IN CERTAIN CANCERS
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-775-920-136

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	Query Match	95.2%	Score 282.8;	DB 19;	Length 1076;
	Best Local Similarity	99.3%;	Pred. No. 6.3e-80;		
	Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	2	CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGTCAGTGCCCATGCAGT	61		
Db	98	CAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGTCAGTGCCCATGCAGT	157		
Qy	62	TTGTCAAAGTGGGGTACTTCTCTCATTCGACGCGCGGTTGTGGTCTTTGGTCTTCGGTTTC	121		
Db	158	TTGTCAAAGTGGGGTACTTCTCTCATTCGACGCGCGGTTGTGGTCTTTGGTCTTCGGTTTC	217		
Qy	122	TGGGCTGCTATGGTGCTAAGACTCAGAGCAAGTGTGCCCTCGTGACGGTCTTCTTCATCC	181		
Db	218	TGGGCTGCTATGGTGCTAAGACTCAGAGCAAGTGTGCCCTCGTGACGGTCTTCTTCATCC	277		
Qy	182	TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGTGGTCCCTTGGTGACACCAAA	241		
Db	278	TCCTCCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGTGGTCCCTTGGTGACACCAAA	337		
Qy	242	TGGCTGAGCACTTCCCGACGGTTGCTGGTAGTGCCCTGGCCATCAAGAA	287		
Db	338	TGGCTGAGCACTTCCCGACGGTTGCTGGTAGTGCCCTGGCCATCAAGAA	383		

RESULT 13
US-10-097-340-323
; Sequence 323, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAWATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen Lu
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149

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; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-323
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RESULT 14
US-10-205-823-422
; Sequence 422, Application US/10205823
; Publication No. US2003010893A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746

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	5	247.8	94.9	1373	9	BC001291 Homo sapi
	6	244.6	93.7	1028	9	AJ001348 Homo sapi
	7	125.6	48.1	2724	9	AK092545 Homo sapi
	8	124.4	47.7	100079	9	AC108002 Homo sapi
	9	124.4	47.7	105156	2	AF235094 Homo sapi
	10	124.4	47.7	153005	2	AC011976 Homo sapi
C	11	124.4	47.7	157839	2	AC015718 Homo sapi
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	13	121.2	46.4	103247	2	AF176678 Homo sapi
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15	37.2	14.3	643	10	BC049723 Mus musc	
C	16	36.4	13.9	228208	2	AC119786 Rattus no
	17	36.4	13.9	262875	2	AC120775 Rattus no
	18	36.2	13.9	216132	2	AC151012 Callithri
	19	35.6	13.6	399	6	AR417479 Sequence

/note="unnamed protein product; protein sequence is in
conflict with the conceptual translation"
/codon_start=1
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/db_xref="GI:673355"

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LLEPMPFFYLCKIRYCNLEGPPIINSVFKEYAGSMGSCGGLWLAIIALLASIA
GLSL"

ORIGIN

Query Match 94.9%; Score 247.8; DB 6; Length 1026;
Best Local Similarity 97.3%; Pred. No. 8.5e-69;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 62
DB 522 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 581

QY 63 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 122
DB 582 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 641

QY 123 CGTGAATAATTTCCACGTTTTTCATGTTTCCGACAGGTGCTCGCTGGTGTGCACG 182
DB 642 CGTGAATAATTTCCACGTTTTTCATGTTTCCGACAGGTGCTCGCTGGTGTGCACG 701

QY 183 GATGGAGACACCAAGCCAGGAGAGAGAGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 702 GATGGAGACACCAAGCCAGGAGAGAGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 761

QY 243 TTACCTCAAGTGTGTGAAA 261
DB 762 TTACCTCAAGTGTGTGAAA 780

RESULT 5

BC001291
LOCUS
DEFINITION Homo sapiens cDNA for differentially expressed Col6 gene, mRNA
(cDNA clone IMAGE:3457263), partial cds.

ACCESSION

BC001291

VERSION

BC001291.1 GI:12654892

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1373)

Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klauser, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

TITLE

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1373)

Straussberg, R.

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Direct Submission

Submitted (11-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 4 Row: 1 Column: 23

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 24308142.

FEATURES

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/clone="IMAGE:3457263"

/tissue_type="Cervix, carcinoma"

/clone_lib="NIH MGC_12"

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/note="Vector: PCMV-SPORT6"

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LWLAIIALLASIAAGLSLS"

ORIGIN

Query Match 94.9%; Score 247.8; DB 9; Length 1373;
Best Local Similarity 97.3%; Pred. No. 8.5e-69;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 62
DB 136 CCAGCGAAGCGGACGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 195

QY 63 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 122
DB 196 TTTTCGAGTCCAGAACCCAGGAGGTGCAATAGAGTGGTGTCTGCTGTGGAGAGAGAAACAC 255

QY 123 CGTGAATAATTTCCACGTTTTTCATGTTTCCGACAGGTGCTCGCTGGTGTGCACG 182
DB 256 CGTGAATAATTTCCACGTTTTTCATGTTTCCGACAGGTGCTCGCTGGTGTGCACG 315

QY 183 GATGGAGACACCAAGCCAGGAGAGAGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 316 GATGGAGACACCAAGCCAGGAGAGAGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 375

QY 243 TTACCTCAAGTGTGTGAAA 261
DB 376 TTACCTCAAGTGTGTGAAA 394

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RESULT 6
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LOCUS      HSJ001348      1028 bp      mRNA      linear      PRI 10-FEB-1999
DEFINITION Homo sapiens cDNA for differentially expressed COL6 gene.
ACCESSION  AJ001348
VERSION     AJ001348.1  GI:2407910
KEYWORDS   COL6 gene.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1028)
AUTHORS     Machl,A.W., Plantzter,S.A., Rueckels,M. and Kubbies,M.
TITLE       Identification and characterization of a novel cDNA not expressed
            in Fanconi anemia fibroblasts and B-cell lines
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1028)
AUTHORS     Machl,A.W.
TITLE       Direct Submission
JOURNAL     Submitted (12-SEP-1997) Machl A.W., TR-BY1, Boehringer Mannheim
            GmbH, Nonnenwald 2, 82377 Penzberg, GERMANY
FEATURES   Location/Qualifiers
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             /db_xref="taxon:9606"
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Matches 250; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGCATGCTTGTGAGAGAGAAAACAC 62
DB 522 CCAGCGAACGGACGAGGGTGACAATAGACGCGTGTGTCATGTTGTGAGAGAGAAAACAC 581
QY 63 TTTTCAGTCCCAAGCCCAAGCAGGTGCAATGCGACAGCCATACCTCGGTTATAGCGGC 122
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QY 183 GATGAGAGACCCCAAGCCCAAGGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 702 GATGAGAGACCCCAAGCCCAAGGAGGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 761
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DB 762 TTACCTCAAGTGTGTAAA 780
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DEFINITION Homo sapiens cDNA FLJ35226 fis, clone PROST2001138, moderately
            similar to Homo sapiens cDNA for differentially expressed COL6
            gene.
ACCESSION  AK092545
VERSION     AK092545.1  GI:21751165
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
            Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
            Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
            Nagahari,K., Murakami,K., Yaeuda,T., Iwayanagi,T., Wagatsuma,M.,
            Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
            Kikkawa,E., Omura,Y., Abe,K., Kamiyama,K., Katsuta,N., Sato,K.,
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            Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,
            Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,
            Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
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            Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
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            Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
            Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
            Complete sequencing and characterization of 21,243 full-length
            human cDNAs
            Nat. Genet. 36 (1), 40-45 (2004)
            14702039
            2
            Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
            Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
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            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
            NEDO human cDNA sequencing project
            Unpublished
            3 (bases 1 to 2724)
            Isogai,T. and Yamamoto,J.
            Direct Submission
            Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
            Karusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
            NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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FEATURES

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Matches 140; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 3 CCAGCCAAAGGAGGAGGACAAATAGAGTGGTTCATGCTGTGAGAGAGAAAACAC 62
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QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATAGCTGGTATAGCGGC 122
Db 209 TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATAGCTGGTATAGCGGC 268
QY 123 CGTGAATAATTTCCAGCTTTTTCATGTTTCCACAGAGTCT 166
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RESULT 8

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LOCUS Homo sapiens chromosome 8, clone CTD-2292P10, complete sequence.
DEFINITION AC108002
ACCESSION AC108002.3 GI:19225055
VERSION HTG.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100079)
Homo sapiens chromosome 8, clone CTD-2292P10, complete sequence.
Unpublished
2 (bases 1 to 100079)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Brown, A., Camarata, J., Chang, J., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Hughes, M., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Lander, E., Leach, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., McKernan, K., Meidrim, J., Meneus, C., Miho, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24583
Center clone name: 2292_P10

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TITLE

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N.,
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Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
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Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 59705 59804: gap of unknown length
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* 95523 95622: gap of unknown length
* 95623 98567: contig of 2945 bp in length
* 98568 98667: gap of unknown length
* 98668 101380: contig of 2713 bp in length
* 101381 101480: gap of unknown length
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FEATURES

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RESULT 10

AC011976

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LOCUS          AC011976          153005 bp      DNA      linear      HTG 13-MAY-2001
DEFINITION     Homo sapiens clone RP11-15018, WORKING DRAFT SEQUENCE, 5 unordered
pieces.

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ACCESSION AC011976

VERSION AC011976.5 GI:11560232

KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 153005)

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AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

TITLE Homo sapiens, clone RP11-15018

JOURNAL Unpublished

AUTHORS 2 (bases 1 to 153005)

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Castle, A., Cawley, M., Collins, S., Collymore, A.,
Cooke, P., DeArelano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferrel, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

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McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 6, 2000 this sequence version replaced gi:7341825.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L3500

Center clone name: 15_O18

----- Summary Statistics
Sequencing vector: M13; M77815; 41% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 151299 bases at least Q40

Consensus quality: 151929 bases at least Q30

Insert size: 133000; agarose-fp

Quality coverage: 10.5 in Q20 bases; agarose-fp

Quality coverage: 9.2 in Q20 b.

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 59733 59832: gap of 100 bp

* 59833 62883: contig of 3051 bp in length

* 62884 62983: gap of 100 bp

* 62984 67564: contig of 4581 bp in length

* 67565 67664: gap of 100 bp

* 67665 121673: contig of 54009 bp in length

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FEATURES

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RESULT 11
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 DEFINITION Homo sapiens clone RP11-119A16, 4 unordered pieces.
 AC015718
 ACCESSION
 VERSION
 HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 AUTHORS

REFERENCE
 1 (bases 1 to 157839)
 Homo sapiens chromosome, clone RP11-119A16
 Unpublished
 2 (bases 1 to 157839)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
 Baldwin, J., Barna, N., Beckerly, R., Boguslavskiy, L., Boukhgalter, B.,
 Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A.,
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 Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
 Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testafaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
 Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 157839)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B.,
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
 Chospel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,
 Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
 Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
 McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
 Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
 Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Testafaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
 JOURNAL
 COMMENT

Direct Submission
 Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 9, 2002 this sequence version replaced gi:14029953.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

 Center: Whitehead Institute/ MIT Center for Genome Research
 Genome Center
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence submissions@genome.wi.mit.edu

 Project Information
 Center project name: L1404
 Center clone name: 119_A_16

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 7973: contig of 7973 bp in length
 * 7974 8073: gap of 100 bp
 * 8074 81857: contig of 73784 bp in length
 * 81858 81957: gap of 100 bp
 * 81958 136278: contig of 54321 bp in length
 * 136279 136378: gap of 100 bp
 * 136379 157839: contig of 21461 bp in length.

FEATURES
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 /db_xref="taxon:9606"
 /clone="RP11-119A16"
 /clone_lib="RPC1-11 Human Male BAC"

ORIGIN

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 Best Local Similarity 95.5%; Pred. No. 8.7e-29;
 Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 Db 41082 AAATATTTCCAGTGTTCATGTTTCGCAACAGGTGCTCCGCTCGTGTGTCAGCGATGG 41141
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QY 188 AGAGACCCAGCCAGAGAGAGCGGTTCTCTCGAAGAGCCCATGCCCTCTTTTACC 247
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 Db 41202 TCAAGTGTGTGTA 41215
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RESULT 12
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 LOCUS
 DEFINITION Homo sapiens chromosome 8, clone RP11-706C16, complete sequence.
 AC083841
 ACCESSION
 VERSION
 HTG: AC083841.9 GI:21206312
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 1 (bases 1 to 203375)
 Homo sapiens chromosome 8, clone RP11-706C16, complete sequence.
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Unpublished
 2 (bases 1 to 203375)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepe, Y., Colangelo, M., Collins, S., Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mieng, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivat, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougne, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

TITLE
Submitted (03-OCT-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL

3 (bases 1 to 203375)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepe, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

TITLE
Submitted (03-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL

4 (bases 1 to 203375)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepe, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

JOURNAL

Submitted (25-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2002 this sequence version replaced gi:20303671.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submission@genome.wi.mit.edu
----- Project Information
Center project name: L11315
Center clone name: 706_C16

FEATURES

source

Location/Qualifiers

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Query Match 47.7%; Score 124.4; DB 9; Length 203375;

Best Local Similarity 95.5%; Pred. No. 8.7e-29;

Matches 128; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 248 TCAAGTGTGTGTA 261
D 184619 TCAAGTGTGTGTA 184606
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RESULT 13

AF176678

LOCUS AF176678 Homo sapiens chromosome 8 clone CTA-93D7 map 8q24.3, WORKING DRAFT
DEFINITION SEQUENCE, 13 unordered pieces.

ACCESSION AF176678

VERSION AF176678.3 GI:14277241

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 103247)

AUTHORS Schilhabel,M.B., Baumgart,C., Dette,M., Jahn,N.,
Lehmann,R., Menzel,U., Polley,A., Reichwald,K., Schudy,A.,

Siddiqui,R., Taudien,S., Wen,G., Schlegelberger,B., Siebert,R.,
Rosenthal,A. and Platzner,M.
Chromosome 8 genomic sequence
Unpublished
2 (bases 1 to 103247)
Polley,A., Wen,G., Baumgart,C., Dette,M., Jahn,N., Schilhabel,M.,
Menzel,U. and Rosenthal,A.
Direct Submission
Submitted (09-AUG-1999) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
On Jun 1, 2001 this sequence version replaced gi:8151715.

----- Genome Center
Center: Insitute of Molecular Biotechnology
Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
----- Project Information
Center project name: H187
Center clone name: CTA-93D7
----- Summary Statistics

Sequencing vector: M13; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 98831 bases at least Q40
Consensus quality: 94832 bases at least Q30
Consensus quality: 98334 bases at least Q20
Coverage: 5.01 in Q20 bases; sum-of-contigs

Sequence Quality Assessment:

This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1 1510: contig of 1510 bp in length
* 1511 1610: gap of unknown length
* 1611 4022: contig of 2412 bp in length
* 4023 4122: gap of unknown length
* 4123 8486: contig of 4364 bp in length
* 8487 8586: gap of unknown length
* 8587 12803: contig of 4217 bp in length
* 12804 12903: gap of unknown length
* 12904 16146: contig of 3243 bp in length
* 16147 16246: gap of unknown length
* 16247 23920: contig of 7674 bp in length
* 23921 24021: gap of unknown length
* 24021 29710: contig of 5690 bp in length
* 29711 29810: gap of unknown length
* 29811 33268: contig of 3458 bp in length
* 33269 33368: gap of unknown length
* 33369 42999: contig of 9531 bp in length
* 42999 43000: gap of unknown length
* 43000 54681: contig of 11682 bp in length
* 54682 60929: contig of 6148 bp in length
* 60930 61029: gap of unknown length
* 61030 79991: contig of 18962 bp in length
* 79992 80091: gap of unknown length
* 80092 103247: contig of 23156 bp in length.
* Location/Qualifiers
* 1..103247
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FEATURES
source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 Location/Qualifiers
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ORIGIN
Query Match      14.3%; Score 37.2; DB 10; Length 643;
Best Local Similarity 53.4%; Pred. No. 1.2;
Matches 78; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy  37  TGTCTATGCTTGTGAGAGAGAAACACTTTCGAGTGCACCAAGGAGGTGCAATGG 96
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Qy  97  ACAGAGCCATCTGCGTTATAGCGCGGTGAAATATTTCCACGTTTTTTTCATGTTGCG 156
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Qy  157  AACAGGTGCTCGCGTGTGTCAGC 182
Db  244  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    244  AACAGTGCACCCGAGGTTCCAC 269
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Search completed: August 27, 2005, 09:49:26
Job time : 1389.39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:08:44 ; Search time 2434.6 Seconds
(without alignments)
4080.665 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 261

Sequence: 1 agccgcgaacgacgagg.....tttacctcaagtgtgtaaa 261

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	247.8	94.9	560	1	AI583197 tq64g09.x
3	247.8	94.9	560	1	AI703260 wd82b10.x
4	247.8	94.9	575	2	BE551234 7b56d09.x
5	247.8	94.9	619	1	AI828018 wf12f09.x
6	247.8	94.9	640	4	BG492128 602535267
7	247.8	94.9	647	4	BG027935 602294533
8	247.8	94.9	679	5	BM915575 AGENCOURT
9	247.8	94.9	682	5	BQ676087 AGENCOURT
10	247.8	94.9	682	5	BQ679186 AGENCOURT
11	247.8	94.9	684	5	BU500474 AGENCOURT
12	247.8	94.9	909	5	BQ276968 AGENCOURT
13	247.8	94.9	2326	3	CR590427 full-length
14	246.2	94.3	626	2	BE547043 601076162
15	245.2	93.9	636	4	BI560005 603253476
16	240.2	92.0	1042	5	BE546303 601071161
17	236.8	90.7	664	2	BE546303 601071161
18	235.2	90.1	807	4	BG491699 602535536
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25	210.2	80.5	1100	4	BM555598	BM555598 AGENCOURT
C 26	206.8	79.2	691	4	BG492263	BG492263 602535536
C 27	200	76.6	542	2	BE670388	BE670388 7e34b04.x
C 28	199.4	76.4	447	2	BE466210	BE466210 h227d11.x
C 29	188.4	72.2	295	2	AW518819	AW518819 ha43609.x
C 30	181.4	69.5	441	4	BG110594	BG110594 602281046
C 31	179.2	68.7	675	2	BF718611	BF718611 KEST82.no
C 32	177.4	68.0	999	5	BM911850	BM911850 AGENCOURT
C 33	174.2	66.7	1070	4	BM554262	BM554262 AGENCOURT
C 34	171.2	65.6	482	1	AI740834	AI740834 wg24g04.x
C 35	165.8	63.5	422	1	AI081839	AI081839 ov24a06.x
C 36	164.4	63.0	517	7	W44613	W44613 zc29d04.r1
C 37	152	58.2	187	2	BE937764	BE937764 PM2-TN002
C 38	146.2	56.0	439	2	AW450430	AW450430 UI-H-BI3-
C 39	146.2	56.0	1112	4	BM808520	BM808520 AGENCOURT
C 40	127.8	49.0	394	2	AW445220	AW445220 UI-H-BI3-
C 41	126.8	48.6	463	1	AI860440	AI860440 wk92606.x
C 42	126.8	48.6	857	5	BU543716	BU543716 AGENCOURT
C 43	126.8	48.6	984	5	BQ942376	BQ942376 AGENCOURT
C 44	126.6	48.5	377	1	AA723706	AA723706 ah85e02.s
C 45	125.4	48.0	378	1	AI674656	AI674656 wd18h02.x

ALIGNMENTS

RESULT 1
BE550793
LOCUS
DEFINITION
7b59a07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3232500 3', similar to TR:O15227 O15227 CDNA FOR DIFFERENTIALLY EXPRESSED COL6 GENE ; mRNA sequence.
ACCESSION
BE550793
VERSION
BE550793.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 559)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 487.
Location/Qualifiers
1..559
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3232500"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI CGAP Lu5 was prepared and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo. "

Query Match 94.9%; Score 247.8; DB 2; Length 559;
 Best Local Similarity 97.3%; Pred. No. 1.9e-68;
 Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGATCGGACGAGGAGTGAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 62
 |||||
 Db 277 CCAGCGAAGCGGACGAGGAGTGAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 336
 |||||

QY 63 TTTCGAGTCCGAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 122
 |||||
 Db 337 TTTCGAGTCCGAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 396
 |||||

QY 123 CGTGAATAATTTCCACAGTTTTCATGTTTCGCAACAGGCTCGCTGGTGTGTCAGC 182
 |||||
 Db 397 CGTGAATAATTTCCACAGTTTTCATGTTTCGCAACAGGCTCGCTGGTGTGTCAGC 456
 |||||

QY 183 GATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCATGCCCTTCTT 242
 |||||
 Db 457 GATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCATGCCCTTCTT 516
 |||||

QY 243 TTACCTCAAGTGTGTAA 261
 |||||
 Db 517 TTACCTCAAGTGTGTAA 535
 |||||

RESULT 2
 AI583197
 LOCUS
 DEFINITION
 tq64g09.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2213632 3',
 similar to TR:O15227 O15227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16
 GENE.; mRNA sequence.

ACCESSION
 AI583197
 VERSION
 1
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 560)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

JOURNAL
 COMMENT
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 463.
 Location/Qualifiers
 1..560
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2213632"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Lu19"
 /notes="Organ: Lung; Vector: p7T73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 pooled lung tumor tissue, and was then primed with a Not I

- oligo(dT) primer. Double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 p7T73 vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.
 Fatima Bonaldo. "

ORIGIN

Query Match 94.9%; Score 247.8; DB 1; Length 560;
 Best Local Similarity 97.3%; Pred. No. 1.9e-68;
 Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGACGAGGAGTGAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 62
 |||||
 Db 263 CCAGCGAACGACGAGGAGTGAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 322
 |||||

QY 63 TTTCGAGTCCGAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 122
 |||||
 Db 323 TTTCGAGTCCGAGAACCCAGGAGGTGCAATAGAGTGGTGTCTATGCTGTGAGAGAGAAACAC 382
 |||||

QY 123 CGTGAATAATTTCCACAGTTTTCATGTTTCGCAACAGGCTCGCTGGTGTGTCAGC 182
 |||||
 Db 383 CGTGAATAATTTCCACAGTTTTCATGTTTCGCAACAGGCTCGCTGGTGTGTCAGC 442
 |||||

QY 183 GATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCATGCCCTTCTT 242
 |||||
 Db 443 GATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCATGCCCTTCTT 502
 |||||

QY 243 TTACCTCAAGTGTGTAA 261
 |||||
 Db 503 TTACCTCAAGTGTGTAA 521
 |||||

RESULT 3
 AI703260
 LOCUS
 DEFINITION
 wd82b10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2338075 3',
 similar to TR:O15227 O15227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16
 GENE.; mRNA sequence.

ACCESSION
 AI703260
 VERSION
 1
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 560)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

JOURNAL
 COMMENT
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 461.
 Location/Qualifiers
 1..560
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2338075"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu24"

FEATURES
 source

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match	94.9%;	Score 247.8;	DB 1;	Length 560;
Best Local Similarity	97.3%;	Pred. No. 1.9e-68;		
Matches 252;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 3 CCAGCGAACGGACGGGTGCAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 62
 DB 263 CCAGCGAACGGACGGGTGCAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 322
 QY 63 TTTCGAGTGCCAGAACCCCAAGGAGTGCATAATGGACAGAGCCATCTCGGTTTATAGCGGC 122
 DB 323 TTTCGAGTGCCAGAACCCCAAGGAGTGCATAATGGACAGAGCCATCTCGGTTTATAGCGGC 382
 QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 182
 DB 383 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 442
 QY 183 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
 DB 443 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 502
 QY 243 TTACCTCAAGTGTGTAAA 261
 DB 503 TTACCTCAAGTGTGTAAA 521

RESULT 4

BE551234
 LOCUS 7b56d09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:323241 3'
 DEFINITION similar to TR:O15227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16 GENE.; mRNA sequence.
 ACCESSION BE551234
 VERSION BE551234.1 GI:972926
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 575)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: -40UP from Gibco
 High quality sequence stop: 507.
 Location/Qualifiers
 1. 575
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:323241"
 /tissue_type="carcinoid"

FEATURES

source

FEATURES

source

1. 619
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2350409"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

/lab_host="DH10B"

/clone_lib="NCI CGAP Lu24"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match	94.9%;	Score 247.8;	DB 2;	Length 575;
Best Local Similarity	97.3%;	Pred. No. 1.9e-68;		
Matches 252;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY 3 CCAGCGAACGGACGGGTGCAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 62
 DB 284 CCAGCGAACGGACGGGTGCAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACAC 343
 QY 63 TTTCGAGTGCCAGAACCCCAAGGAGTGCATAATGGACAGAGCCATCTCGGTTTATAGCGGC 122
 DB 344 TTTCGAGTGCCAGAACCCCAAGGAGTGCATAATGGACAGAGCCATCTCGGTTTATAGCGGC 403
 QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 182
 DB 404 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCAGC 463
 QY 183 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
 DB 464 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 523
 QY 243 TTACCTCAAGTGTGTAAA 261
 DB 524 TTACCTCAAGTGTGTAAA 542

RESULT 5

AI828018
 LOCUS wf12f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350409 3', similar to TR:O15227 O15227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16 GENE.; mRNA sequence.
 ACCESSION AI828018
 VERSION AI828018.1 GI:5448610
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 619)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the Inert Consortium (info@image.llnl.gov) for further information.
 Inert Length: 845 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 467.
 Location/Qualifiers
 1. 619
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2350409"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBh19w, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made *in vitro*. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 297480-302087, 682632-689739, 726408-728711, and 723096-731399. Subtraction by Bento Soares and M. Patina Bonaldo.

ORIGIN

Query Match	94.9%;	Score 247.8;	DB 1;	Length 619;
Best Local Similarity	97.3%;	Prod. No. 1.9e-68;		
Matches 252;	Conservative	0; Mismatches 7;	Indels 0;	Gaps 0;
3	CCAGCGAACGGACGAGGGGTGACAAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAAACAC	62		
263	CCAGCGAACGGACGAGGGGTGACAAATAGAGTGTGGTGTGTCATGTTTGTGAGAGAGAAACAC	322		
63	TTTTCAGTGCAGAACCCNAGGAGGTGCAATATGGACAGAGCCATACTCGTTATAGCGGC	122		
323	TTTTCAGTGCAGAACCCNAGGAGGTGCAATATGGACAGAGCCATACTCGTTATAGCGGC	382		
123	CGTGAATAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTGTGTGCAGC	182		
383	CGTGAATAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTGTGTGCAGC	442		
183	GATGAGAGACCCAGCCAGAGGAGNAGGGTTTCTCTGGNAGAGCCCATGCCCTTCTT	242		
443	GATGAGAGACCCAGCCAGGAGGAGCGGTTTCTCTGGNAGAGCCCATGCCCTTCTT	502		
243	TTACCTCAAGTGTGTGAAA	261		
503	TTACCTCAAGTGTGTGAAA	521		

RESULT 6

Accession	BC492128	640 bp	linear	EST 27-MAR-2001
LOCUS	602535267T1	NIH_MGC_41	Homo sapiens cDNA clone IMAGE:4654072 3',	
DEFINITION	mRNA sequence.			
ACCESSION	BC492128			
VERSION	BC492128.1	GI:13453640		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 640)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg. Ph.D.			

FEATURES

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1. .640
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4654072"
/tissue_type="amelanotic"
/lab host="DH10B (phage-
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/clone lib="NIH MGC 41"
note="organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAC(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using Zap-M cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

```

ORIGIN

Query Match	94.9%;	Score 247.8;	DB 4;	Length 640;
Best Local Similarity	97.3%;	Pred. No. 2e-68;		
Matches 252;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0
Qy	3	CCACGCGAACCGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGTGAGAGAGAGAAAAACAC	62	
Db	452	CCACGCGAACCGACGAGGGTGACAATAGAGTGTGGTGTGTCATGTTTGTGAGAGAGAGAAAAACAC	393	
Qy	63	TTTTCGAGTGCAGAACCCGACGAGGTTGCAAAATGGACAGAGCCATACTGGGTTATAGCGC	122	
Db	392	TTTTCGAGTGCAGAACCCGACGAGGTTGCAAAATGGACAGAGCCATACTGGTATTATAGCGC	333	
Qy	123	CGTCAAAATAATTCCACAGTTTTTTCATGGTTTCGCAACAGGTGCTCCGCTGGTGTGTGCAGC	182	
Db	332	CGTCAAAATAATTCCACAGTTTTTTCATGGTTTCGCAAGCAGTGTCTCCGCTGGTGTGTGCAGC	273	
Qy	183	GATCGAGAGCCCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT	242	
Db	272	GATCGAGAGACCCCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT	213	
Qy	243	TTACCTCAAGTGTGTGAAA	261	
Db	212	TTACCTCAAGTGTGTGAAA	194	

RESULT 7

BG027935	602294533f1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389033 5', linear mRNA 647 bp	EST 24-JAN-2000
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

FEATURES

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Location/Qualifiers
1. .647
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4389033"
/tissue_type="osteosarcoma,
/lab_host="DH10B (phage-res
/clone_lib="NH_MGC_86"
/note="Organ: bone; Vector:
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library."

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ORIGIN
Query Match          94.9%; Score 247.8; DB 4; Length 647;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      3   CCAGCGAACGGAGCGAGGGTGACAAATAGAGTGTGGTGTGCATGCTTGTGAGAGAGAAAACAC 62
      |||
Db      138  CCAGCGAACGGAGCGAGGGTGACAAATAGAGTGTGGTGTGCATGCTTGTGAGAGAGAAAACAC 197
      |||

QY      63   TTTTCGAGTGCAGAACCCCAAGGAGGTGCCAAATGGACAGAGCCATCTGCGTTATAGCGGC 122
      |||
Db      198  TTTTCGAGTGCAGAACCCCAAGGAGGTGCCAAATGGACAGAGCCATCTGCGTTATAGCGGC 257
      |||

QY      123  CGTGAATAATTTCCACGTTTTTTTCATGTTTCGCAACACAGGTGCTCGCGCTGGTTGTGCAGC 182
      |||
Db      258  CGTGAATAATTTCCACGTTTTTTTCATGTTTGGAGCAGTGTCTCCGCTGGTTGTGCAGC 317
      |||

QY      183  GATGGAGAGACCCAAGCCAGAGGAGAAAGCGGTTTCTCTGGAAGAGGCCATGCCCTTCCT 242
      |||
Db      318  GATGGAGAGACCCAAGCCAGAGGAGAAAGCGGTTTCTCTGGAAGAGGCCATGCCCTTCCT 377
      |||

QY      243  TTACCTCAAGTGTGTAA 261
      |||
Db      378  TTACCTCAAGTGTGTAA 396
      |||

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RESULT 8	BM915575	679 bp	linear	EST 12-MAR-2002
LOCUS	AGENCOURT_6701603	NIH_MGC_41	Homo sapiens	cDNA clone IMAGE:5481773
DEFINITION	5', mRNA sequence.			
ACCESSION	BM915575			
VERSION	BM915575.1	GI:19365954		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 679)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Straubeberg, Ph.D.			
	Email: cgabbs@mail.nih.gov			
	Tissue Procurement: DCTD/DTP			
	CDNA Library Preparation: Rubin Laboratory			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: LLCM2006	row: m	column: 06	
	High quality sequence stop: 680.			

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FEATURES
source
high quality sequence stop: 880.
Location/Qualifiers
1. .679
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5481773"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DHI0B (phage-resistant)"
/clone_lib="NIH MGC 41"
/notes="Organ: skin; Vector: pOTB7; Site 1: xhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/xhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

```

Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

ORIGIN	Query Match	94.9%	Score 247.8;	DB 5;	Length 679;
	Best Local Similarity	97.3%;	pred. No. 2e-68;		
	Matches 252;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	3	CCAGCGAACGGAGCGAGGGTGACAATAGATGTGTGGTGTGATGCTTGTGAGAGAGAAACAC	62		
Db	165	CCAGCGAACGGAGCGAGGGTGACAATAGATGTGTGGTGTGATGCTTGTGAGAGAGAAACAC	224		
Qy	63	TTTTCGAGTGCAGAACCCACGAGGAGGTGCAATAGGACAGAGCCCATACTGCGTTTATAGCGGC	122		
Db	225	TTTTCGAGTGCAGAACCCACGAGGAGGTGCAATAGGACAGAGCCCATACTGCGTTTATAGCGGC	284		
Qy	123	CGTGAATAATTTCCACGTTTTTTTCATGGTTTCACAACAGGTGCTCGCTCGTTGTGTCAGC	182		
Db	285	CGTGAATAATTTTCACGTTTTTTTCATGGTTTCGAGACGAGTGCTCCGCTGGTTGTGTCAGC	344		
Qy	183	GATGGAGAGACCCAAAGCCAGAGGAGAAGCGGTTTCTCTGGAAAGAGCCCATGCCCTTCTT	242		
Db	345	GATGGAGAGACCCAAAGCCAGAGGAGAAGCGGTTTCTCTGGAAAGAGCCCATGCCCTTCTT	404		
Qy	243	TTACCTCAAGTGTGTGATAA	261		
Db	405	TTACCTCAAGTGTGTGATAA	423		

RESULT 9	
BQ676087	
LOCUS	
DEFINITION	BQ676087 682 bp mRNA linear EST 15-JUL-2002 AGENCOURT 8507940 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294463 5', mRNA sequence.
ACCESSION	BQ676087
VERSION	BQ676087.1 GI:21788766
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 682)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2499 row: c column: 08 High quality sequence stop: 637.

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FEATURES
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1. .682
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6294463"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GACACAG(C)G. Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

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ORIGIN
Query Match          94.9%; Score 247.8; DB 5; Length 682;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGAGAGAGAAAACAC 62
DB 157 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGAGAGAGAAAACAC 216
QY 63 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATGAGAGCCATCTGCGTTATAGCGGC 122
DB 217 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATGAGAGCCATCTGCGTTATAGCGGC 276
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTGTGCGAGC 182
DB 277 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTGTGCGAGC 336
QY 183 GATGGAGAGACCCCAAGCCAGAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 337 GATGGAGAGACCCCAAGCCAGAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 396
QY 243 TTAACCTCAAGTGTGTGTA 261
DB 397 TTAACCTCAAGTGTGTGTA 415

RESULT 10
BQ679186
LOCUS
DEFINITION BQ679186 682 bp mRNA linear EST 15-JUL-2002
5', mRNA sequence.
ACCESSION BQ679186
VERSION BQ679186
KEYWORDS BQ679186.1 GI:21791865
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2333 row: j column: 06
High quality sequence stop: 660.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6091109"
/tissue_type="melanotic melanoma, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match          94.9%; Score 247.8; DB 5; Length 684;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGAGAGAGAAAACAC 62
DB 157 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGAGAGAGAAAACAC 216
QY 63 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATGAGAGCCATCTGCGTTATAGCGGC 122
DB 217 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATGAGAGCCATCTGCGTTATAGCGGC 276
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTGTGCGAGC 182
DB 277 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTGTGCGAGC 336
QY 183 GATGGAGAGACCCCAAGCCAGAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 337 GATGGAGAGACCCCAAGCCAGAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 396
QY 243 TTAACCTCAAGTGTGTGTA 261
DB 397 TTAACCTCAAGTGTGTGTA 415

RESULT 11
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LOCUS
DEFINITION BQ679186 684 bp mRNA linear EST 12-SEP-2002
5', mRNA sequence.
ACCESSION BQ679186
VERSION BQ679186
KEYWORDS BQ679186.1 GI:22801450
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: NIMH/LOG
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2355 row: e column: 11
High quality sequence start: 2
High quality sequence stop: 648.
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/notes="Vector: pOTB7a; Site 1: CeuI; Site 2: ScaI; This
library is a size selection of NIH_MGC_35, from 3.0-4.5
kb. Size selection done at the National Institute of
Mental Health, NIH. Note: this is a NIH_MGC Library."

ORIGIN
Query Match          94.9%; Score 247.8; DB 5; Length 684;
Best Local Similarity 97.3%; Pred. No. 2e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGAGAGAGAAAACAC 62
DB 157 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTGTCATGCTTGAGAGAGAAAACAC 216
QY 63 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATGAGAGCCATCTGCGTTATAGCGGC 122
DB 217 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATGAGAGCCATCTGCGTTATAGCGGC 276
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTGTGCGAGC 182
DB 277 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGAGTGCTCCGCTGTGTGCGAGC 336
QY 183 GATGGAGAGACCCCAAGCCAGAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 337 GATGGAGAGACCCCAAGCCAGAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 396
QY 243 TTAACCTCAAGTGTGTGTA 261
DB 397 TTAACCTCAAGTGTGTGTA 415
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Db      144 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 203
QY      63 TTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 122
Db      204 TTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 263
QY      123 CGTGAAAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 182
Db      264 CGTGAAAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 323
QY      183 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db      324 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 383
QY      243 TTACCTCAAGTGTGTGAAA 261
Db      384 TTACCTCAAGTGTGTGAAA 402

RESULT 12
LOCUS   BQ276968
DEFINITION AGENCOURT_6770142 NIH_MGC_126 Homo sapiens cDNA clone IMAGE:5810055
5', mRNA sequence.
ACCESSION BQ276968
VERSION   BQ276968.1 GI:20487176
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2056 row: k column: 16
High quality sequence stop: 505.
Location/Qualifiers
1. .909
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/mol_type="mRNA"
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/clone="IMAGE:5810055"
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/lab_host="PH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site 1: SfiI (gcccattagcc);
Site 2: SfiI (ggcgctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAAGCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT
5'-ATTCTAGAGCGCGCCGACATG-TT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

FEATURES source
1. .909
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5810055"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="PH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_126"
/note="Vector: pDNR-LIB; Site 1: SfiI (gcccattagcc);
Site 2: SfiI (ggcgctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAAGCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT
5'-ATTCTAGAGCGCGCCGACATG-TT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 94.9%; Score 247.8; DB 3; Length 2326;
Best Local Similarity 97.3%; Pred. No. 2.8e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 62
Db 123 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 182
QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 122
Db 183 TTTCGAGTGCAGAACCCAGGAGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 242
QY 123 CGTGAAAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 182
Db 264 CGTGAAAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTGTGTCAGC 323
QY 183 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 324 GATGGAGAGACCCAGCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 383
QY 243 TTACCTCAAGTGTGTGAAA 261
Db 384 TTACCTCAAGTGTGTGAAA 402

RESULT 13
LOCUS   CR590427
DEFINITION full-length cDNA clone CSODK010YP02 of HeLa cells Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR590427
VERSION   CR590427.1 GI:50471234
KEYWORDS HTC; CNSLT_cDNA.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 2326)
Direct Submision
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .2326
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK010YP02"
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ORIGIN
Query Match 94.9%; Score 247.8; DB 3; Length 2326;
Best Local Similarity 97.3%; Pred. No. 2.8e-68;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 62
Db 165 CCAGCGAACCGGACGAGGGTGCAATAGAGTGTGGTGTCTATGTTGTGAGAGAGAAACAC 224

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QY 63 TTTCGAGTCCAGAACCCAGAGAGGTGCAATGGACAGAGCCATACCTCGTTATAGCGGC 122
DB 225 TTTCGAGTCCAGAACCCAGAGAGGTGCAATGGACAGAGCCATACCTCGTTATAGCGGC 284
QY 123 CGTGAATAATATTCACAGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
DB 285 CGTGAATAATATTCACAGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 344
QY 183 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTTCTT 242
DB 345 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTTCTT 404
QY 243 TTACCTCAAGTGTGTAA 261
DB 405 TTACCTCAAGTGTGTAA 423

RESULT 14
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DEFINITION 601076162F1 NTH_MGC_12 Homo sapiens cDNA clone IMAGE:3462278 5',
mRNA sequence.
ACCESSION BE547043
VERSION BE547043.1 GI:9775779
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 626)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8459 row: k column: 15
High quality sequence stop: 585.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3462278"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/note="Organ: Cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."

ORIGIN
Query Match 94.3%; Score 246.2; DB 2; Length 626;
Best Local Similarity 96.9%; Pred. No. 6.4e-68;
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 62
DB 130 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 189
QY 63 TTTCGAGTCCAGAACCCAGAGAGGTGCAATGGACAGAGCCATACCTCGTTATAGCGGC 122
DB 190 TTTCGAGTCCAGAACCCAGAGAGGTGCAATGGACAGAGCCATACCTCGTTATAGCGGC 249
QY 123 CGTGAATAATATTCACAGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182

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DB 250 CGTGAATAATATTCACAGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 309
QY 183 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTTCTT 242
DB 310 GATGAGAGACCCAGCCAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTTCTT 369
QY 243 TTACCTCAAGTGTGTAA 261
DB 370 TTACCTCAAGTGTGTAA 388

RESULT 15
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DEFINITION 603253476F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295811 5',
mRNA sequence.
ACCESSION BI560005
VERSION BI560005.1 GI:15447319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 636)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM411748 row: h column: 20
High quality sequence stop: 636.
Location/Qualifiers
1..636
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5295811"
/lab_host="DH10B"
/clone_lib="NIH MGC 97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
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insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

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Query Match 93.9%; Score 245.2; DB 4; Length 636;
Best Local Similarity 96.9%; Pred. No. 1.3e-67;
Matches 250; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 62
DB 114 CCAGCGAACCGAGCGGTGACAATAGAGTGGTGTCTCATGCTGTGAGAGAGAAAACAC 173
QY 63 TTTCGAGTCCAGAACCCAGAGAGGTGCAATGGACAGAGCCATACCTCGTTATAGCGGC 122
DB 174 TTTCGAGTCCAGAACCCAGAGAGGTGCAATGGACAGAGCCATACCTCGTTATAGCGGC 233
QY 123 CGTGAATAATATTCACAGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182

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[illegible]

Search completed: August 27, 2005, 11:16:23
Job time : 2437.6 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 08:38:03 ; Search time 478.968 Seconds
(without alignments)
3565.473 Million cell updates/sec

Title: US-10-079-954-2
Perfect score: 261
Sequence: 1 agccagcgaacgacgagg.....tttacctcaagtgtgtaaa 261

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261	100.0	261	13	US-10-079-954-2
2	247.8	94.9	672	17	Sequence 2, Appli
3	247.8	94.9	672	18	Sequence 339, App
4	247.8	94.9	754	17	Sequence 172, App
5	247.8	94.9	754	17	Sequence 172-832-172
6	247.8	94.9	1026	9	Sequence 2414, Ap
7	247.8	94.9	1026	14	Sequence 2414, Ap
					Sequence 1, Appli
					Sequence 1, Appli

RESULT 1

US-10-079-954-2
; Sequence 2, Application US/10079954
; Publication No. US20020168661A1
; GENERAL INFORMATION:
; APPLICANT: Durst, Matthias
; APPLICANT: Nees, Matthias
; TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
; FILE REFERENCE: SCHU 204 (09902857)
; CURRENT APPLICATION NUMBER: US/10/079,954
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US/09/308,984
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/DE97/02660
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: DE 196 49207
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-954-2

ALIGNMENTS

8	247.8	94.9	1373	17	US-10-295-027-753	Sequence 753, App
9	246.2	94.3	502	17	US-10-264-049-1723	Sequence 1723, Ap
10	233.6	89.5	1745	20	US-10-723-860-7232	Sequence 7232, Ap
11	34.8	13.3	417	14	US-10-238-443-13	Sequence 13, Appl
12	34.8	13.3	417	15	US-10-309-362-13	Sequence 13, Appl
13	34.8	13.3	627	14	US-10-238-443-11	Sequence 11, Appl
14	34.8	13.3	627	15	US-10-309-362-11	Sequence 11, Appl
15	34.8	13.3	1710	14	US-10-238-443-10	Sequence 10, Appl
16	34.8	13.3	1710	15	US-10-309-362-10	Sequence 10, Appl
17	34.8	13.3	3676	14	US-10-238-443-3	Sequence 3, Appli
18	34.8	13.3	3676	15	US-10-309-362-3	Sequence 3, Appli
19	34.8	13.3	3715	17	US-10-443-108-1	Sequence 1, Appli
20	33.8	13.0	1260	17	US-10-188-646-4	Sequence 4, Appli
21	33.8	13.0	1268	19	US-10-807-897-28	Sequence 28, Appl
22	33.8	13.0	1322	19	US-10-807-897-26	Sequence 26, Appl
23	33.8	13.0	1337	14	US-10-235-026-1	Sequence 1, Appli
24	33.8	13.0	1363	20	US-10-839-882-37	Sequence 37, Appl
25	33.8	13.0	1376	14	US-10-244-586-1	Sequence 1, Appli
26	33.8	13.0	4810	17	US-10-188-646-11	Sequence 11, Appl
27	32.6	12.5	458	14	US-10-184-644-496	Sequence 496, App
28	32.6	12.5	458	14	US-10-184-634-496	Sequence 496, App
29	32	12.3	170	22	US-10-651-991-90	Sequence 90, Appl
30	31.2	12.0	651	19	US-10-767-701-2245	Sequence 2245, Ap
31	31.2	12.0	114793	22	US-10-148-806-3	Sequence 3, Appli
32	31.2	12.0	114793	22	US-10-859-792-3	Sequence 3, Appli
33	31	11.9	637	13	US-10-027-632-255637	Sequence 255637,
34	31	11.9	637	17	US-10-027-632-255637	Sequence 19, Appl
35	31	11.9	2142	9	US-09-989-722-19	Sequence 19, Appl
36	31	11.9	2142	9	US-09-989-723-19	Sequence 19, Appl
37	31	11.9	2142	9	US-09-989-727-19	Sequence 19, Appl
38	31	11.9	2142	9	US-09-989-727-19	Sequence 19, Appl
39	31	11.9	2142	9	US-09-989-731-19	Sequence 19, Appl
40	31	11.9	2142	9	US-09-989-732-19	Sequence 19, Appl
41	31	11.9	2142	9	US-09-991-073-19	Sequence 19, Appl
42	31	11.9	2142	9	US-09-991-073-19	Sequence 19, Appl
43	31	11.9	2142	9	US-09-991-163-19	Sequence 19, Appl
44	31	11.9	2142	9	US-09-993-604-19	Sequence 19, Appl
45	31	11.9	2142	9	US-09-990-456-19	Sequence 19, Appl

Query Match 100.0%; Score 261; DB 13; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1e-82;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGCCAGCGAACGAGCGAGGGTGACAATAGAGTGTGGTGTATGCTGTGTGAGAGAGAAAC 60
Qy 61 ACTTTTCGAGTCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGG 120
Db 61 ACTTTTCGAGTCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGG 120
Qy 121 GCCGTGMAAATATTTCACGTTTTTTCATGTTTTCGCAACAGAGTGTCTCGCTGTTGTGCA 180
Db 121 GCCGTGMAAATATTTCACGTTTTTTCATGTTTTCGCAACAGAGTGTCTCGCTGTTGTGCA 180
Qy 181 GCGATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTC 240
Db 181 GCGATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTC 240
Qy 241 TTTTACCTCAAGTGTGTAA 261
Db 241 TTTTACCTCAAGTGTGTAA 261

RESULT 2

US-10-295-027-339
; Sequence 339, Application US/10295027
; Publication No. US2003032350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-339

Query Match 94.9%; Score 247.8; DB 17; Length 672;
Best Local Similarity 97.3%; Pred. No. 8.5e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 CCAGCGAACGAGCGAGGGTGACAATAGAGTGTGGTGTATGCTGTGTGAGAGAGAAACAC 62

Db 267 CCAGCGAACGAGCGAGGGTGACAATAGAGTGTGGTGTATGCTGTGTGAGAGAGAAACAC 326
Qy 63 TTTTCGAGTCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 122
Db 327 TTTTCGAGTCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 386
Qy 123 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCTCGCTGTTGTGACG 182
Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCTCGCTGTTGTGACG 446
Qy 183 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 447 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
Qy 243 TTACTCAAGTGTGTAA 261
Db 507 TTACTCAAGTGTGTAA 525

RESULT 3

US-10-188-832-172
; Sequence 172, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 172
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-832-172

Query Match 94.9%; Score 247.8; DB 18; Length 672;
Best Local Similarity 97.3%; Pred. No. 8.5e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 3 CCAGCGAACGAGCGAGGGTGACAATAGAGTGTGGTGTATGCTGTGTGAGAGAGAAACAC 62
Db 267 CCAGCGAACGAGCGAGGGTGACAATAGAGTGTGGTGTATGCTGTGTGAGAGAGAAACAC 326
Qy 63 TTTTCGAGTCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 122
Db 327 TTTTCGAGTCCAGAACCCAGGAGGTGCAATATGACAGAGCCATCTACTGCGTTATAGCGGC 386
Qy 123 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCTCGCTGTTGTGACG 182
Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCTCGCTGTTGTGACG 446
Qy 183 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 447 GATGGAGAGACCCAAAGCCAGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
Qy 243 TTACTCAAGTGTGTAA 261

Db 507 TTACCTCAAGTGTGTAAA 525
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RESULT 4
US-10-172-118-2414/c
; Sequence 2414, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2414
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Contig49058
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2414

Query Match 94.9%; Score 247.8; DB 17; Length 754;
Best Local Similarity 97.3%; Pred. No. 8.9e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 62
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Db 498 CCAGCGAACGGACGAGGGTGACANTAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 439
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QY 63 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 122
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Db 438 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 379
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QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTTGTGCAGC 182
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Db 378 CGTGAATAATTTCCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTTGTGCAGC 319
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QY 183 GATGAGAGACCCCAAGCCAGAGAGGAGGCGGTTTCTCTGGAAGAGAGCCCATGCCCTTCTT 242
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Db 318 GATGAGAGACCCCAAGCCAGAGAGGAGGCGGTTTCTCTGGAAGAGAGCCCATGCCCTTCTT 259
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QY 243 TTACCTCAAGTGTGTAAA 261
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Db 258 TTACCTCAAGTGTGTAAA 240
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RESULT 5
US-10-342-887-2414/c
; Sequence 2414, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999

; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2414
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-2414

Query Match 94.9%; Score 247.8; DB 18; Length 754;
Best Local Similarity 97.3%; Pred. No. 8.9e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 62
|||
Db 498 CCAGCGAACGGACGAGGGTGACATAGAGTGTGGTGTCTCATGTGTGAGAGAGAAAACAC 439
|||

QY 63 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 122
|||
Db 438 TTTCGAGTGCCAGAACCCCAAGGAGTGCAATAGGACAGAGCCATAGTGGTTATAGCGGC 379
|||

QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTTGTGCAGC 182
|||
Db 378 CGTGAATAATTTCCACGTTTTTTCATGTTTCCACAGAGTCTCCGCTGGTTGTGCAGC 319
|||

QY 183 GATGAGAGACCCCAAGCCAGAGGAGGCGGTTTCTCTGGAAGAGAGCCCATGCCCTTCTT 242
|||
Db 318 GATGAGAGACCCCAAGCCAGAGGAGGCGGTTTCTCTGGAAGAGAGCCCATGCCCTTCTT 259
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QY 243 TTACCTCAAGTGTGTAAA 261
|||
Db 258 TTACCTCAAGTGTGTAAA 240
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RESULT 6
US-09-977-801-1
; Sequence 1, Application US/09977801
; Publication No. US20020086848A1
; GENERAL INFORMATION:
; APPLICANT: Fanconi-gene II
; TITLE OF INVENTION: Fanconi-gene II
; NUMBER OF SEQUENCES: 2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,801
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,632
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..924
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 430..924
US-09-977-801-1

Query Match	94.9%;	Score 247.8;	DB 9;	Length 1026;
Best Local Similarity	97.3%;	Pred. No. 1e-77;		
Matches 252;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	3	CCAGCGAACGGACGGGTGCAATAGAGTGTGCTGCTCATGCTTGTGAGAGAGAAAAACAC	62	
DB	522	CCAGCGAACGGACGGGTGCAATAGAGTGTGCTGCTCATGCTTGTGAGAGAGAAAAACAC	581	
QY	63	TTTTCGAGTGCACGAACCCAAAGGAGTGCCAAATGGACACAGACCACATCTGCGTTATAGCGCG	122	
DB	582	TTTTCGAGTGCACGAACCCAAAGGAGTGCCAAATGGACACAGACCACATCTGCGTTATAGCGCG	641	
QY	123	CGTGAATAATTTCCACGCTTTTTTCATGGTTTCGCAACAGAGTGCTCGCGTGGTTGTGCAGC	182	
DB	642	CGTGAATAATTTCCACGCTTTTTTCATGGTTTCGCAACAGAGTGCTCGCGTGGTTGTGCAGC	701	
QY	183	GATGAGAGACCCAAAGCCAGAGAGAACGCGTTTCTCTCGAAAGACCATGCCCTTCCT	242	
DB	702	GATGAGAGACCCAAAGCCAGAGAGAACGCGTTTCTCTCGAAAGACCATGCCCTTCCT	761	
QY	243	TTACCTCAAGTGTGTGTAAG	261	
DB	762	TTACCTCAAGTGTGTGTAAG	780	

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RESULT 7
US-10-199-448-1
; Sequence 1, Application US/10199448
; Publication NO. US20030022858A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Mannheim GmbH
; TITLE OF INVENTION: Fanconi-gene II
; NUMBER OF SEQUENCES: 2
; STREET: Sandhofer Str. 112-132
; CITY: Mannheim
; COUNTRY: Germany
; ZIP: 68305
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,448
; FILING DATE: 19-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,801
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/09/402,632
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1026 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256...924
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 430...924
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-199-448-1

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Qy	63	TTTTCGAGTGCAGAAACCAAGGAGGTGCAAAATGGACAGAGCCATAC	TGCGTTATATAGCGC	122
Db	582	TTTTCGAGTGCAGAAACCAAGGAGGTGCAAAATGGACAGAGCCATAC	TGCGTTATATAGCGC	641
Qy	123	CGTGAATAATTTCCACGTTTTTTTCATGGTTTCGAAACAGGTGCTCCGCTGGTTGTGCAGC		182
Db	642	CGTGAATAATTTTCACGTTTTTTTCATGGTTTCGAAACAGGTGCTCCGCTGGTTGTGCAGC		701
Qy	183	GATGGACAGACCCCAAGCCACAGGAGAGACGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT		242
Db	702	GATGGACAGACCCCAAGCCACAGGAGAGACGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT		761
Qy	243	TTACCTCAAGTGTGTGTAAA	261	
Db	762	TTACCTCAAGTGTGTGTAAA	780	

RESULT 8
US-10-295-027-753
; Sequence 753, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel

APPLICANT: Ginsberg, Wendy H.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 753
 LENGTH: 1373
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-295-027-753

Query Match	94.9%;	Score 247.8;	DB 14;	Length 1026;
Best Local Similarity	97.3%;	Pred. No. 1e-77;		
Matches 252; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

QY	3	CCAGCGAACGGACGAGGGGTGCATATAGATGTCTGTTCATGCTTGTGAGAGAGAAAACAC	62
Db	522	CCAGCGAACCAGCAGGGGTGCATATAGATGTCTGTTCATGCTTGTGAGAGAGAAAACAC	581

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US-10-255-027-753
Query Match      94.9%; Score 247.8; DB 17; Length 1373;
Best Local Similarity 97.3%; Pred. No. 1.le-77;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0
Qy 3 CCACCGAACCGACGAGGGTGACAATAGAGTGTGGTGTTCATGCTTGTGAGAGAGAAACAC 62

```

```

QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 122
Db 196 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 255
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCAGC 182
Db 256 CGTGAATAATTTCCACGTTTTTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCAGC 315
QY 183 GATGGAGAGACCAACGAGGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 316 GATGGAGAGACCAACGAGGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 375
QY 243 TTACCTCAAGTGTGTAAA 261
Db 376 TTACCTCAAGTGTGTAAA 394

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RESULT 9

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US-10-264-049-1723
; Sequence 1723, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/19569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1723
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-1723

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```

Query Match 94.3%; Score 246.2; DB 17; Length 502;
Best Local Similarity 96.9%; Pred. No. 2.8e-77;
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAGAAACAC 62
Db 85 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAGAAACAC 144
QY 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 122
Db 145 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGTTATAGCGGC 204
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCAGC 182
Db 205 CGTGAATAATTTCCACGTTTTTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCAGC 264
QY 183 GATGGAGAGACCAACGAGGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 265 GATGGAGAGACCAACGAGGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 324
QY 243 TTACCTCAAGTGTGTAAA 261
Db 325 TTACCTCAAGTGTGTAAA 343

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RESULT 10

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US-10-723-860-7232
; Sequence 7232, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert

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; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators &
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7232
; LENGTH: 1745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7232

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```

Query Match 89.5%; Score 233.6; DB 20; Length 1745;
Best Local Similarity 96.2%; Pred. No. 1.5e-72;
Matches 250; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 3 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAGAAACAC 62
Db 507 CCAGCGAACGGACGAGGTGCAATAGAGTGTGCTCATGCTTGTGAGAGAGAAACAC 566
QY 63 -TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGCTTATAGCGG 121
Db 567 TTTCGAGTGCAGAACCCAGGAGGTGCAATGGACAGAGCCATCTCGCTTATAGCGG 626
QY 122 CGTGAATAATTTCCACGTTTTTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCAG 181
Db 627 CGTGAATAATTTCCACGTTTTTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCAG 686
QY 182 CGATGGAGAGACCAACGAGGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCT 241
Db 687 CGATGGAGAGACCAACGAGGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCT 746
QY 242 TTACCTCAAGTGTGTAAA 261
Db 747 TTACCTCAAGTGTGTAAA 766

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RESULT 11

```

US-10-238-443-13
; Sequence 13, Application US/10238443
; Publication No. US20030083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/198,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 13
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-238-443-13

```

```

Query Match 13.3%; Score 34.8; DB 14; Length 417;
Best Local Similarity 57.3%; Pred. No. 0.12;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 84 GAGGTGCAAAATGGACAGAGCCATCTCGTTATAGCGGCGCGTGAATAATTTCCACGTTT 143
Db 220 GGGATGGGAGTGGATAAAGCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 279
QY 144 TTTCATGTTTCCAAACAGGTCTCCGCTGGTTGTGCGAGCGGATGGAGAGAC 193
Db 280 ATGGCTGGGTACTACCAAGAGTCTGCGCGGCGTGGCGGATGGAGAGCC 329

```

```
RESULT 12
US-10-309-362-13
; Sequence 13, Application US/10309362
; Publication No. US20030114412A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/309,362
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 13
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: unknown
US-10-309-362-13

Query Match      13.3%; Score 34.8; DB 15; Length 417;
Best Local Similarity 57.3%; Pred. No. 0.12;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy      84 GAGGTGCAATGGACAGAGCCATCTCGGTTATAGCGCGCGTGAATAATTTCCACGTTT 143
Db      220 GGGATGGGAGTGGATAAAGCAATGTCAGGTTTGTGCGCCCATTTGGAATATTTGCCAAGTCT 279

Qy      144 TTTCATGGTTCCCAACAGGTGCTCGGTTGTGTCAGCATGGAGAGAC 193
Db      280 ATGGCTGGGTACTACCAAGAGTCTGCGCGGGCTGGCAGGGATGGGAAGCC 329

RESULT 13
US-10-238-443-11
; Sequence 11, Application US/10238443
; Publication No. US2003083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 11
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 330
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 360
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 394
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 440
; OTHER INFORMATION: unknown

RESULT 14
US-10-309-362-11
; Sequence 11, Application US/10309362
; Publication No. US20030114412A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/309,362
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 11
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 330
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 360
; OTHER INFORMATION: unknown
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 465
; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 557
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 580
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 595
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-10-238-443-11

Query Match      13.3%; Score 34.8; DB 14; Length 627;
Best Local Similarity 57.3%; Pred. No. 0.14;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy      84 GAGGTGCAATGGACAGAGCCATCTCGGTTATAGCGCGCGTGAATAATTTCCACGTTT 143
Db      100 GGGATGGGAGTGGATAAAGCAATGTCAGGTTTGTGCGCCCATTTGGAATATTTGCCAAGTCT 159

Qy      144 TTTCATGGTTCCCAACAGGTGCTCGGTTGTGTCAGCATGGAGAGAC 193
Db      160 ATGGCTGGGTACTACCAAGAGTCTGCGCGGGCTGGCAGGGATGGGAAGCC 209

RESULT 14
US-10-309-362-11
; Sequence 11, Application US/10309362
; Publication No. US20030114412A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/309,362
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 11
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 330
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 360
; OTHER INFORMATION: unknown
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```
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 388
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 394
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
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; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
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; OTHER INFORMATION:
US-10-309-362-11
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Query Match      13.3%; Score 34.8; DB 15; Length 627;
Best Local Similarity 57.3%; Pred. No. 0.14;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      84 GAGGTGCAATGGACAGAGCCATCTGCGTTATAGCGCGCGTGAATAATTTCCACGTTT 143
Db      100 GGGATGGGAGTGGATAAAGCCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 159

QY      144 TTTCATGGTTTCCCAACAGGTGCTCCGCTGTTGTGCGAGGATGGAGAGAC 193
Db      160 ATGGCTGGGTACTACAGGAGTCTGCGCGGCTGGCAGGGATGGGAAGCC 209
```

```
RESULT 15
US-10-238-443-10
; Sequence 10, Application US/10238443
; Publication No. US2003083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
```

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; SEQ ID NO 10
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-238-443-10
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Query Match      13.3%; Score 34.8; DB 14; Length 1710;
Best Local Similarity 57.3%; Pred. No. 0.21;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      84 GAGGTGCAATGGACAGAGCCATCTGCGTTATAGCGCGCGTGAATAATTTCCACGTTT 143
Db      1085 GGGATGGGAGTGGATAAAGCCCAATGTCAGGTTTGTGCGCCCATTTGGAATATTGCCAAGTCT 1144

QY      144 TTTCATGGTTTCCCAACAGGTGCTCCGCTGTTGTGCGAGGATGGAGAGAC 193
Db      1145 ATGGCTGGGTACTACAGGAGTCTGCGCGGCTGGCAGGGATGGGAAGCC 1194
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Search completed: August 27, 2005, 11:33:35
Job time : 479.968 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 07:00:48 ; Search time 311.984 Seconds
(without alignments)
4952.347 Million cell updates/sec

Title: US-10-079-954-2
Perfect score: 261
Sequence: 1 agccagcaagcagcaggg.....tttacctcaagtggtgtaaa 261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.2	98.2	261	2 AAV15589	AAV15589 Human HPK
2	247.8	94.9	672	8 ACC51042	ACC51042 Human bla
3	247.8	94.9	672	8 ABX76400	ABX76400 Lung canc
4	247.8	94.9	672	11 ADN39021	ADN39021 Cancer/an
5	247.8	94.9	754	13 ADR26553	ADR26553 Breast ca
6	247.8	94.9	775	10 ADF60035	ADF60035 Human con
7	247.8	94.9	775	13 ADQ511654	ADQ511654 Human the
8	247.8	94.9	1026	2 AAV64572	AAV64572 Human Fan
9	247.8	94.9	1373	6 ABK92263	ABK92263 Prostate
10	247.8	94.9	1373	8 ABX76167	ABX76167 Lung canc
11	247.8	94.9	1373	11 ADN39435	ADN39435 Cancer/an
12	247.8	94.9	1705	13 ADQ87331	ADQ87331 Human tum
13	246.2	94.3	502	6 ABQ55843	ABQ55843 Human ova
14	233.6	89.5	1745	12 ADQ24412	ADQ24412 Human sof
15	175.8	67.4	748	13 ADS10353	ADS10353 Human the
16	137.8	52.8	516	10 ADF58395	ADF58395 Human pol
17	35.6	13.6	1065	4 AAS40959	AAS40959 cDNA enco
18	34.8	13.3	439	4 AAG41516	AAG41516 cDNA enco
19	34.8	13.3	1108	2 AA231913	AA231913 Human hel
20	34.8	13.3	1183	2 AA231920	AA231920 Human hel

21	34.8	13.3	1740	4 AAK94445	AAK94445 Human ful
22	34.8	13.3	1740	12 ADL31205	ADL31205 Full leng
23	34.8	13.3	1749	4 AAF87638	AAF87638 Human Rec
24	34.8	13.3	3159	13 ACN42473	ACN42473 Human dia
25	34.8	13.3	3703	4 AAF87636	AAF87636 Human Rec
26	34.8	13.3	3703	13 ADR83444	ADR83444 Human Rec
27	34.8	13.3	3707	2 AA231910	AA231910 Human hel
28	34.8	13.3	3715	4 AAF87637	AAF87637 Human Rec
29	34.8	13.3	3715	12 ADF83094	ADF83094 Human Rec
30	34.8	13.3	3879	13 ACN40275	ACN40275 Tumour-as
31	33.8	13.0	1260	12 ADH89535	ADH89535 Human Liv
32	33.8	13.0	1268	10 ACC72844	ACC72844 Human can
33	33.8	13.0	1268	13 ADS71346	ADS71346 Human liv
34	33.8	13.0	1322	10 ACC72843	ACC72843 Human can
35	33.8	13.0	1322	13 ADG71344	ADG71344 Human liv
36	33.8	13.0	1337	3 AAZ61210	AAZ61210 DNA enco
37	33.8	13.0	1363	3 AAA15007	AAA15007 cDNA enco
38	33.8	13.0	1376	4 AAF24856	AAF24856 Nucleotid
39	33.8	13.0	4810	12 ADH89542	ADH89542 Human Liv
c 40	33.6	12.9	2984	4 ABL25052	ABL25052 Drosophil
c 41	32	12.3	2000	8 ADA71938	ADA71938 Rice gene
42	31.8	12.2	2813	12 ADH10681	ADH10681 Mouse CX3
43	31.8	12.2	110000	12 ADN46845_05	Continuation (6 of
c 44	31.8	12.2	110000	12 ADN47591_15	Continuation (16 of
45	31.8	12.2	110000	12 ADN46123_05	Continuation (6 of

ALIGNMENTS

RESULT 1

AAV15589
ID AAV15589 standard; DNA; 261 BP.

AC AAV15589;

DT 02-JUL-1998 (first entry)

DE Human HPK-1A C21.7 DNA.

KW Cervical cancer; treatment; diagnosis; passage cell; lesion;
human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

OS Homo sapiens.

PN DE19649207-C1.

PD 26-FEB-1998.

PF 27-NOV-1996; 96DE-01049207.

PR 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Duerst M, Nees M;

XX WPI; 1998-121623/12.

PT Nucleic acid characteristic of late or early passage cells immortalised
by papilloma virus - and related polypeptide(s) and antibodies, used for
diagnosis and treatment of cervical cancer and assessing potential for
progression of cervical lesions.

XX Claim 3; Fig 2; 8pp; German.

XX This sequence, C21.7, is derived from a human papillomavirus (HPV)
immortalised human foreskin keratinocyte cell line HPK-1A and is
characteristic of late or early passage cells. This sequence is used in a
method for assessing the potential for progression of cervical lesions.
XX Antibodies generated against the encoded polypeptide are used for
diagnosis of cervical cancer and to assess potential for lesion
progression. Antibodies can also be used therapeutically by inhibiting

PA	(EOSB-) EOS BIOTECHNOLOGY INC.	KW	inflammatory disease; autoimmune disease;
XX		KW	retinal neovascularisation syndrome; scarring; uterine fibroid;
XX	Aziz N, Murray R;	KW	detection; diagnosis; prognosis; drug screening; drug targeting;
XX		KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;
DR	WPI: 2003-093161/08.	XX	vulnerary; gene therapy; vaccine; gene; ss.
DR	P-PSDB; ABUS6671.	OS	Homo sapiens.
PT	Detecting a lung cancer-associated transcript in a cell from a patient	XX	
PT	for treating lung cancer, by contacting a biological sample from the	XX	
PT	patient with a polynucleotide that exhibits increased or decreased	PN	WO2003042661-A2.
PT	expression in lung cancer.	XX	
XX		PD	22-MAY-2003.
PS	Claim 22; Page 392; 453pp; English.	XX	
XX		PF	13-NOV-2002; 2002WO-US036810.
CC	The invention relates to a method for detecting a lung cancer-associated	XX	
CC	transcript in a cell from a patient, comprising contacting a biological	PR	13-NOV-2001; 2001US-0350666P.
CC	sample from the patient with a polynucleotide that selectively hybridises	PR	21-NOV-2001; 2001US-0332464P.
CC	to a sequence that is at least 80 % identical to a gene that exhibits	PR	29-NOV-2001; 2001US-0334393P.
CC	increased or decreased expression in lung cancer samples. Lung cancer-	PR	03-DEC-2001; 2001US-0335394P.
CC	associated polynucleotides and polypeptides are used for identifying a	PR	14-DEC-2001; 2001US-0340376P.
CC	compound that modulates a lung cancer-associated polypeptide, for	PR	08-JAN-2002; 2002US-0347211P.
CC	inhibiting proliferation of a lung cancer-associated cell to treat lung	PR	10-JAN-2002; 2002US-0347349P.
CC	cancer in a patient and for treating a mammal having lung cancer by	PR	08-FEB-2002; 2002US-0355250P.
CC	administering a modulatory compound identified. The methods are useful	PR	13-FEB-2002; 2002US-0356714P.
CC	for treating lung cancer, such as small cell lung cancer, non-small cell	PR	20-FEB-2002; 2002US-0359077P.
CC	lung cancer or other benign or precancerous lesions, e.g. atelectasis,	PR	29-MAR-2002; 2002US-0368809P.
CC	emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,	PR	04-APR-2002; 2002US-0370110P.
CC	hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and	PR	12-APR-2002; 2002US-0372246P.
CC	bronchiectasis. The genes, polynucleotides and polypeptides are useful	PR	05-JUN-2002; 2002US-0386614P.
CC	for diagnostic purposes and as targets for screening for therapeutic	PR	16-JUL-2002; 2002US-0396839P.
CC	compounds that modulate lung cancer, such as antibodies. Sequences	PR	22-JUL-2002; 2002US-0397757P.
CC	ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the	PR	22-JUL-2002; 2002US-0397845P.
CC	invention	PR	09-SEP-2002; 2002US-0409450P.
XX		XX	(EOSB-) EOS BIOTECHNOLOGY INC.
XX	Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;	PA	
SQ		XX	
Query Match	94.9%; Score 247.8; DB 8; Length 672;	PI	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
Best Local Similarity	97.3%; Pred. No. 9.5e-74;	PI	Mack DR, Murray R, Watson SR, Wilson KE, Zlotnik A;
Matches 252; Conservative	0; Mismatches 7; Indels 0; Gaps 0;	XX	
QY	3 CCAGCGAACGGACGGGTGACAAATAGAGTGTGTCTCATGCTGTGAGAGAGAAACAC 62	XX	
DB	267 CCAGCGAACGGACGGGTGACAAATAGAGTGTGTCTCATGCTGTGAGAGAGAAACAC 326	XX	
QY	63 TTTCGAGTCCAGAACCCAGAGGTTGCAATAGAGTGTGTCTCATGCTGTGAGAGAGAAACAC 122	XX	
DB	327 TTTCGAGTCCAGAACCCAGAGGTTGCAATAGAGTGTGTCTCATGCTGTGAGAGAGAAACAC 386	XX	
QY	123 CCGTAAATATTTCCACGTTTTTTTCATGTTTCCGACAGGTGCTCGCTGGTTGTCAGC 182	XX	
DB	387 CCGTAAATATTTCCACGTTTTTTTCATGTTTCCGACAGGTGCTCGCTGGTTGTCAGC 446	XX	
QY	183 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGGCCCATGCCCTTCTT 242	XX	
DB	447 GATGAGAGACCCAGCCAGAGAGAGCGGTTTCTCTGGAAGGCCCATGCCCTTCTT 506	XX	
QY	243 TTACCTCAAGTGTGTGAAA 261	XX	
DB	507 TTACCTCAAGTGTGTGAAA 525	XX	
RESULT 4		XX	
ID	ADN39021	XX	
AC	ADN39021 standard; cDNA; 672 BP.	XX	
DT	17-JUN-2004 (first entry)	XX	
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:339.	XX	
XX		XX	
KW	Human; differential expression; cancer; angiogenic disorder;	XX	
KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;	XX	

KW	inflammatory disease; autoimmune disease;	KW	retinal neovascularisation syndrome; scarring; uterine fibroid;
KW	detection; diagnosis; prognosis; drug screening; drug targeting;	KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW	vulnerary; gene therapy; vaccine; gene; ss.	XX	
OS	Homo sapiens.	XX	
XX		XX	
PN	WO2003042661-A2.	XX	
XX		XX	
PD	22-MAY-2003.	XX	
XX		XX	
PF	13-NOV-2002; 2002WO-US036810.	XX	
XX		XX	
PR	13-NOV-2001; 2001US-0350666P.	XX	
PR	21-NOV-2001; 2001US-0332464P.	XX	
PR	29-NOV-2001; 2001US-0334393P.	XX	
PR	03-DEC-2001; 2001US-0335394P.	XX	
PR	14-DEC-2001; 2001US-0340376P.	XX	
PR	08-JAN-2002; 2002US-0347211P.	XX	
PR	10-JAN-2002; 2002US-0347349P.	XX	
PR	08-FEB-2002; 2002US-0355250P.	XX	
PR	13-FEB-2002; 2002US-0356714P.	XX	
PR	20-FEB-2002; 2002US-0359077P.	XX	
PR	29-MAR-2002; 2002US-0368809P.	XX	
PR	04-APR-2002; 2002US-0370110P.	XX	
PR	12-APR-2002; 2002US-0372246P.	XX	
PR	05-JUN-2002; 2002US-0386614P.	XX	
PR	16-JUL-2002; 2002US-0396839P.	XX	
PR	22-JUL-2002; 2002US-0397757P.	XX	
PR	22-JUL-2002; 2002US-0397845P.	XX	
PR	09-SEP-2002; 2002US-0409450P.	XX	
XX	(EOSB-) EOS BIOTECHNOLOGY INC.	XX	
XX		XX	
PI	Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;	PI	Mack DR, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX		XX	
XX	WPI: 2003-468649/44.	XX	
DR	P-PSDB; ADN39022.	XX	
XX		XX	
PT	Determining the presence or absence of a pathological cell in a patient,	PT	useful for diagnosing, prognosing or treating cancer, comprises detecting
PT	a nucleic acid in a biological sample.	PT	
XX		XX	
PS	Claim 8; SEQ ID NO 339; 1385pp; English.	XX	
XX		XX	
CC	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)	CC	whose expression is upregulated or downregulated in specific cancers or
CC	other diseases such as angiogenic or fibrotic disorders, and to methods	CC	of determining the presence or absence of a pathological cell in a
CC	patient by detecting a nucleic acid at least 80% identical to those of	CC	the invention or by detecting a polypeptide of the invention. The
CC	invention also relates to expression vectors and host cells comprising a	CC	nucleic acid of the invention; antibodies which specifically bind a
CC	polypeptide of the invention; use of such antibodies for drug targeting;	CC	and methods of screening for modulators of activity or expression of the
CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,	CC	antibodies and methods are useful for diagnosing, prognosing and treating
CC	cancer and other conditions such as psoriasis, ischaemia, heart disease,	CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC	neovascularisation syndromes, scarring and uterine fibroids. They may	CC	also be useful in wound healing and in contraception. The present
CC	sequence represents a nucleic acid sequence of the invention.	CC	
XX		XX	
SQ	Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;	XX	
Query Match	94.9%; Score 247.8; DB 11; Length 672;	XX	
Best Local Similarity	97.3%; Pred. No. 9.5e-74;	XX	
Matches 252; Conservative	0; Mismatches 7; Indels 0; Gaps 0;	XX	
QY	3 CCAGCGAACGGACGGGTGACAAATAGAGTGTGTCTCATGCTGTGAGAGAGAAACAC 62	QY	3 CCAGCGAACGGACGGGTGACAAATAGAGTGTGTCTCATGCTGTGAGAGAGAAACAC 62

Db 267 CCAGCGAAGCGAGCGGTGACAAATAGAGTGTGGTGTATGTTTGTGAGAGAGAAACAC 326
QY 63 TTTCAGTGCAGAACCCCAAGAGGTGCAATGGACAGACCATCTCGTTATAGCGGC 122
Db 327 TTTCAGTGCAGAACCCCAAGAGGTGCAATGGACAGACCATCTCGTTATAGCGGC 386
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
Db 387 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 446
QY 183 GATGAGAGACCCCAAGCGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 447 GATGAGAGACCCCAAGCGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
QY 243 TTACTCAAGTGTGTAA 261
Db 507 TTACTCAAGTGTGTAA 525

RESULT 5
ADR26553/c
ID ADR26553 standard; DNA; 754 BP.
XX AC ADR26553;
XX DT 21-OCT-2004 (first entry)
XX DE Breast cancer prognosis marker #2414.
XX KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX OS Homo sapiens.
XX PN WO2004065545-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US001100.
XX PR 15-JAN-2003; 2003US-00342887.
XX PA (ROSE-) ROSETTA INPHARMATICS LLC.
XX PA (NECA-) NETHERLANDS CANCER INST.
XX PI Van't Veer LJ, He Y;
XX DR WPI; 2004-593473/57.
XX CC Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX PS Disclosure; SEQ ID NO 2414; 226pp; English.
XX CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
SQ Sequence 754 BP; 150 A; 245 C; 206 G; 153 T; 0 U; 0 Other;

Query Match 94.9%; Score 247.8; DB 13; Length 754;
Best Local Similarity 97.3%; Pred. No. 1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAAGCGAGCGGTGACAAATAGAGTGTGGTGTATGTTTGTGAGAGAGAAACAC 62
|||||

Db 498 CCAGCGAAGCGAGCGGTGACAAATAGAGTGTGGTGTATGTTTGTGAGAGAGAAACAC 439
QY 63 TTTCAGTGCAGAACCCCAAGAGGTGCAATGGACAGACCATCTCGTTATAGCGGC 122
Db 438 TTTCAGTGCAGAACCCCAAGAGGTGCAATGGACAGACCATCTCGTTATAGCGGC 379
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
Db 378 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 319
QY 183 GATGAGAGACCCCAAGCGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 318 GATGAGAGACCCCAAGCGAGGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTCTT 259
QY 243 TTACTCAAGTGTGTAA 261
Db 258 TTACTCAAGTGTGTAA 240

RESULT 6
ADF60035
ID ADF60035 standard; cDNA; 775 BP.
XX AC ADF60035;
XX DT 12-FEB-2004 (first entry)
XX DE Human contig polynucleotide sequence SEQ ID NO:2402.
XX KW biological activity; genetic engineering; hybridisation probe; oligomer;
KW primer; chromosome mapping; gene mapping; recombinant protein production;
KW human; gene; ss.
XX OS Homo sapiens.
XX PN WO2003080795-A2.
XX PD 02-OCT-2003.
XX PF 09-AUG-2002; 2002WO-US025485.
XX PR 09-AUG-2001; 2001US-0311261P.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Yang Y, Wang Z, Weng G, Ma Y;
XX DR WPI; 2003-876918/81.
XX DR P-PSDB; ADF60487.
XX CC New polynucleotides, useful as hybridization probes, oligomers or
PT primers, for chromosome or gene mapping, for the recombinant production
PT of proteins, and for generating antisense DNA or RNA.
XX Example 2; SEQ ID NO 2402; 571pp; English.
XX CC The present invention describes isolated polynucleotide sequences (I),
CC which encode polypeptides (II) with biological activity. Also described:
CC (1) a vector comprising (I); (2) an expression vector comprising (I); (3)
CC a host cell genetically engineered to comprise (I) which is operatively
CC associated with a regulatory sequence that modulates expression of (I) in
CC the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition
CC comprising the polypeptide of (4) and a carrier; (6) an antibody directed
CC against the polypeptide of (4); (7) detecting (I) or the polypeptide of
CC (4) in a sample; (8) identifying a compound that binds to the polypeptide
CC of (4); (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA. The
CC present sequence represents a human contig polynucleotide sequence, which
CC is used in an example from the present invention.

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SQ Sequence 775 BP; 164 A; 209 C; 250 G; 152 T; 0 U; 0 Other;
Query Match 94.9%; Score 247.8; DB 10; Length 775;
Best Local Similarity 97.3%; Pred. No. 1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTATGCTTGTGAGAGAGAAAACAC 62
DB 267 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTCTATGCTTGTGAGAGAGAAAACAC 326
QY 63 TTTCGAGTCCAGAACCCAAAGGAGTGCATAATGAGAGAGCCCATCTGGTTATAGCGGC 122
DB 327 TTTCGAGTCCAGAACCCAAAGGAGTGCATAATGAGAGAGCCCATCTGGTTATAGCGGC 386
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGAGTCTCCGCTGGTTGTCAGC 182
DB 387 CGTGAATAATTTCCACGTTTTTTCATGTTCCGACAGAGTCTCCGCTGGTTGTCAGC 446
QY 183 GATGAGAGACCCAAAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 447 GATGAGAGACCCAAAGCCAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 506
QY 243 TTACCTCAAGTGTGTGAAA 261
DB 507 TTACCTCAAGTGTGTGAAA 525
RESULT 7
ADSI1654
ID ADSI1654 standard; DNA; 775 BP.
AC ADSI1654;
DT 16-DEC-2004 (first entry)
DE Human therapeutic contig DNA - SEQ ID 1891.
DE antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
OS Homo sapiens.
PN WO2004080148-A2.
XX 23-SEP-2004.
XX 30-SEP-2003; 2003WO-US030720.
PR 02-OCT-2002; 2002US-0416186P.
XX (NUVE-) NUVELO INC.
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
DR WPI; 2004-668857/65.
DR P-PSDB; ADSI2252.
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX Example 2; SEQ ID NO 1891; 718pp; English.
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
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PI cycling or activation, DNA repair, cytopaenia, tumorigenesis etc.
XX Claim 1; Page 18-19; 35pp; German.
PS This sequence encodes a protein which is associated with Fanconi anaemia.
XX This protein can be used as an immunogen for preparation of antibodies.
CC This sequence can be used for diagnosis of, or detecting predisposition
CC to, diseases that involve disorders of the cell cycle, cell activation,
CC cell cycle progression, DNA repair, cytopaenia, tumorigenesis and/or
CC tumour progression, also for treatment and prevention of these diseases,
CC particularly by gene therapy
XX
XX
SQ Sequence 1026 BP; 201 A; 301 C; 331 G; 191 T; 0 U; 2 Other;
Query Match 94.9%; Score 247.8; DB 2; Length 1026;
Best Local Similarity 97.3%; Pred. No. 1.1e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTCTGTCAGAGAGAGAAACAC 62
DB |||||
522 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTCTGTCAGAGAGAGAAACAC 581
QY 63 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAATGGACAGAGCCATCTGCTTATAGCGC 122
DB |||||
582 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAATGGACAGAGCCATCTGCTTATAGCGC 641
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 182
DB |||||
642 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 701
QY 183 GATGAGAGACCCAGCCAGGAGAGAGCGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 702 GATGAGAGACCCAGCCAGGAGAGAGCGTTTCTCTGGAAGAGCCCATGCCCTTCTT 761
QY 243 TTACCTCAAGTGTGTGAAA 261
DB 762 TTACCTCAAGTGTGTGAAA 780
RESULT 9
ABK92263
ID ABK92263 standard; DNA; 1373 BP.
XX
AC ABK92263;
XX
XX 15-AUG-2002 (first entry)
XX Prostate cancer-associated DNA sequence #149.
DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
XX gene therapy/ gene; ds.
XX Mammalia.
XX
XX WO200230268-A2.
PN
XX
PD 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US032045.
PF
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX

PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61944.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 426; 436pp; English.
XX
XX The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1373 BP; 346 A; 324 C; 376 G; 327 T; 0 U; 0 Other;
Query Match 94.9%; Score 247.8; DB 6; Length 1373;
Best Local Similarity 97.3%; Pred. No. 1.3e-73;
Matches 252; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTCTGTCATCTTGTGAGAGAGAAACAC 62
DB |||||
136 CCAGCGAACGGACGAGGGTGACAATAGAGTGGTGTCTGTCATCTTGTGAGAGAGAAACAC 195
QY 63 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAATGGACAGAGCCATCTGCTTATAGCGC 122
DB |||||
196 TTTCGAGTGCCAGAACCCCAAGGAGGTGCAATGGACAGAGCCATCTGCTTATAGCGC 255
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 182
DB |||||
256 CGTGAATAATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTCAGC 315
QY 183 GATGAGAGACCCAGCCAGGAGAGAGCGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 316 GATGAGAGACCCAGCCAGGAGAGAGCGTTTCTCTGGAAGAGCCCATGCCCTTCTT 375
QY 243 TTACCTCAAGTGTGTGAAA 261
DB 376 TTACCTCAAGTGTGTGAAA 394
RESULT 10
ABX76167
ID ABX76167 standard; DNA; 1373 BP.
XX
AC ABX76167;
XX
XX 02-APR-2003 (first entry)
XX Lung cancer-associated polynucleotide #39.
DE Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
XX anti-inflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
OS

ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-147878/19.

P-PSDB; ABP42766.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 1; SEQ ID NO 1723; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 502 BP; 112 A; 125 C; 152 G; 113 T; 0 U; 0 Other;

Query Match 94.3%; Score 246.2; DB 6; Length 502;
Best Local Similarity 96.9%; Pred. No. 2.9e-73;
Matches 251; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

3 CCAGCGACGGACGAGGGTGACAAATAGAGTGTGGTGTCTGCTGTGTGAGAGAGAAACAC 62
DB 85 CCAGCGACGGACGAGGGTGACAAATAGAGTGTGGTGTCTGCTGTGTGAGAGAGAAACAC 144

QY 63 TTTCAGTGCACCAACCAAGGAGTGCATAATGGACAGAGCCATCTCGTTATAGCGGC 122
DB 145 TTTCAGTGCACCAACCAAGGAGTGCATAATGGACAGAGCCGTTACTGGTTATAGCGGC 204
QY 123 CGTGAATAATTTCCACGTTTTTTCATGTTCCGCAACAGGTGCTCCGTGGTGTGACAGC 182
DB 205 CGTGAATAATTTCCACGTTTTTTCATGTTCCGCAACAGGTGCTCCGTGGTGTGACAGC 264
QY 183 GATGGAGAGACCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
DB 265 GATGGAGAGACCAAGCCAGAGGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 324
QY 243 TTACCTCAAGTGTGTAATA 261
DB 325 TTACCTCAAGTGTGTAATA 343

RESULT 14

ADQ24412

ID ADQ24412 standard; DNA; 1745 BP.

AC ADQ24412;

DT 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 7232.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; ds.

OS Homo sapiens.

PN WO2004048938-A2.

PD 10-JUN-2004.

PF 26-NOV-2003; 2003WO-US038193.

PR 26-NOV-2002; 2002US-0429739P.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

PS Example 2; SEQ ID NO 7232; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the CC specification per se but was submitted in CD format by the inventor.

XX Sequence 1745 BP; 402 A; 455 C; 511 G; 377 T; 0 U; 0 Other;

Query Match 89.5%; Score 233.6; DB 12; Length 1745;
Best Local Similarity 96.2%; Pred. No. 9.9e-69;
Matches 250; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 3 CCAGCGAAGCGGAGCGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 62
Db 507 CCAGCGAAGCGGAGCGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 566
Qy 63 -TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATCTGCGTTATAGCGG 121
Db 567 TTTCATATGCGAAGCCAGGAGGTGCAATGACAGAGCCATCTGCGTTATAGCGG 626
Qy 122 CCGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCCGCTGTTGCGAG 181
Db 627 CCGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCCGCTGTTGCGAG 686
Qy 182 CGATGGAGAGCCCAAGCCAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCT 241
Db 687 CGATGGAGAGCCCAAGCCAGGAGGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCT 746
Qy 242 TTACCTCAAGTGTGTATAA 261
Db 747 TTACCTCAAGTGTGTATAA 766

RESULT 15
ADS10353
ID ADS10353 standard; DNA; 748 BP.
XX ADS10353;
AC ADS10353;
DT 16-DEC-2004 (first entry)
DE Human therapeutic DNA - SEQ ID 590.
DE antinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
KW inflammatory; haematopolesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX Homo sapiens.
XX WO2004080148-A2.
XX 23-SEP-2004.
XX 30-SEP-2003; 2003WO-US030720.
XX 02-OCT-2002; 2002US-0416186P.
XX (NUVE-) NUVELO INC.
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
DR P-PSDB; ADS11037.
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX Claim 1; SEQ ID NO 590; 718pp; English.
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX Sequence 748 BP; 157 A; 207 C; 246 G; 138 T; 0 U; 0 Other;

Query Match 67.4%; Score 175.8; DB 13; Length 748;
Best Local Similarity 85.7%; Pred. No. 3.5e-49;
Matches 222; Conservative 0; Mismatches 2; Indels 35; Gaps 1;
Qy 3 CCAGCGAAGCGGAGCGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 62
Db 278 CCAGCGAGCGAGCGAGGTGACAATAGAGTGTGGTGTGATGCTTGTGAGAGAAAACAC 337
Qy 63 TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATCTGCGTTATAGCGG 122
Db 338 TTTCGAGTGCAGAACCCAGGAGGTGCAATGACAGAGCCATCTGCGTTATAGCGG 397
Qy 123 CGTGAATAATTTCCACGTTTTTTCATGTTTTCGCAACAGAGTGTCCGCTGTTGCGAG 182
Db 398 CGTGA-----TGCTCCGCTGTTGCGAG 422
Qy 183 GATGGAGAGACCCCAAGCCAGAGGAGAAAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 423 GATGGAGAGACCCCAAGCCAGAGGAGAAAGCGGTTTCTCTGGAAGAGCCCATGCCCTTCTT 482
Qy 243 TTACCTCAAGTGTGTATAA 261
Db 483 TTACCTCAAGTGTGTATAA 501

Search completed: August 27, 2005, 08:59:49
Job time : 313.984 secs


```
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match      13.6%; Score 35.6; DB 4; Length 399;
Best Local Similarity 12.4%; Pred. No. 0.023;
Matches 29; Conservative 108; Mismatches 97; Indels 0; Gaps 0;

QY 10 ACGACGAGGTGCAATAGATGGTGTCTATGCTGTGAGAGAGAAACCTTTCCGAG 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 40 WKKRRRRRRWWWWKSMCMWKKSKSWRSWGMWTKRMKGRGAASWAGYMSMTYMTTRW 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 TCCAGAACCCAGGAGGTGCAATCGACAGAGCCACTACTGCTTATAGCGCCGTGAA 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 RYIRYRKAKTKWRAAGMGMWKGAGWAMAYAKWYMWARRTAMKYWAMMKSKSRMRRAW 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 ATATTCCACGTTTTTTTTCATGGTTGCCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAG 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 YAWMYMWARRTWGMWRASCYRGAYWASAGMYMWMYMMYMRKMYWSAGWSNWKWTRRC 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 AGACCAACCCAGAGAGAGAGCGGTTCCTCTCGAAGAGCCCATGCCCTCTTTT 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 ASYSCSSSYCMWAKMWMYWKTSRWSYWSYRCTKYRSCCCSMSCWVKTY 273

RESULT 3
US-09-949-016-3456
; Sequence 3456, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3456
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3456

Query Match      13.3%; Score 34.8; DB 4; Length 1233;
Best Local Similarity 57.3%; Pred. No. 0.077;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 84 GAGGTGCAATGACAGAGCCACTACTGCTGTATAGCGCCGTGAAATATTTCCAGTTT 143
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 958 GGGATGGGAGTGGATTAAGCCATGTCAGGTGTGTCGCCCATGGATATTCAGAGTCT 1017
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 TTTTCATGTTGCCAACAGGTGCTCCGCTGTGTGCAGCGATGGAGAGAC 193
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; Patent No. 1018
; Sequence 1018, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1949
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1949

Query Match      13.0%; Score 33.8; DB 4; Length 1260;
Best Local Similarity 53.4%; Pred. No. 0.17;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 94 TGGCAGAGCCACTACTGCTGTATAGCGCCGTGAAATATTTCCACGTTTTTTCATGTT 153
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 151 TGGTCAGAGCCAGGTGTTCCCTCCATGGACCTAAAGACAGTGCACAGTCCACCGTG 210
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 154 CGCAACAGGTCTCCGCTGGTTGTGCAGCGATGGAGACCCAGCCAGAGGAGGCGG 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 211 GACCACAGCCAGCCACTTGGCAGCCGCTGTATGTCACCGAGCGCTGTGACCC 270
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 214 TTTCTCTGGAAG 226
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 271 GCTCTCTGGCAG 283
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-127-928-1
; Sequence 1, Application US/09127928
; Patent No. 6472172
; GENERAL INFORMATION:
; APPLICANT: Deng, Gang
; APPLICANT: Lin, Jiling-Huey
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis
; FILE REFERENCE: Protein
; FILE REFERENCE: DNA Encoding HIAP3
; CURRENT APPLICATION NUMBER: US/09/127,928
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1337
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(1066)
US-09-127-928-1

Query Match      13.0%; Score 33.8; DB 4; Length 1337;
Best Local Similarity 53.4%; Pred. No. 0.18;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
```

94	Qy	TTGACACAGCGCATACGCGTTATAGCGGCGTGAATAATTTCACGTTTTCATCGTT	153
147	Db	TTGTCACAGCGCATGTTTCCCTCATGCGGACCTTAAGACAGTGCCAAAGTGCGTGCACCGTG	206
154	Qy	CGCAACAGGTGCTCCGCTGGTTGTGCGAGCATGGAGAGACCCAAAGCCAGAGGAGAACGG	213
207	Db	GACCAACAGCCGAGCCACTGGGAGCGGTGATGTGTCACGACAGAGCGCTGTGGACCCC	266
214	Qy	TTTCTCCTCGGAAG	226
267	Db	GCTCTCTGGGCAG	279

```

RESULT 6
US-09-949-016-13691
; Sequence 13691, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0601307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13691
; LENGTH: 8572
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13691

```

	Query Match	13.0%	Score 33.8;	DB 4;	Length 8572;
	Best Local Similarity	53.4%;	Pred. No. 0.46;		
	Matches	71;	Conservative	0;	Mismatches 62;
					Indels 0;
					Gaps 0;
Qy	94	TGGACAGAGCCATCTCGGTTATAGCGCGCGTGAARATATTCCACCTTTTTCATCGTT	153		
Db	2151	TGGTCAGAGCCAGTGTTCCTTCCATGGAGCCTAAAGACAGTGCCCAAGTGCTGCACCGTG	2210		
Qy	154	CGCAACAGGTGCTCCGCTGGTGTGTGCAGCGATGGAGAGACCCAAAGCCAGGAGAAAGCGG	213		
Db	2211	GACCACAGCCGAGGCACATGGCGAGCCCGTGTATGTCCACGCAGGAGCGCTGTGGACCCC	2270		
Qy	214	TTTCTCTCTGGAAG	226		
Db	2271	GCTCTCTGGGCAG	2283		

```

RESULT 7
US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; FILE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38

```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3
```

	Query Match	12.0%;	Score 31.2;	DB 4;	Length 114793;
	Best Local Similarity	58.7%;	Pred. No. 14;		
	Matches 54;	Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;
Qy	147	CATGGTTCGCAACAGGTCTCCGCTGGTTGTGCAGGATGGAGAGACCCAGCCAGGAGA	206		
Db	43606	CCTGGTAGGCAACCGAGCGCTCTTTGCCATTGCAGGATGAAGCCACCGAGCGAGGGAGA	43665		
Qy	207	GAAGCGGTTTCTCCTGGAGAGCCCATGCCCCT	238		
Db	43666	AAAGTCTTTGGCCCTACAGCAACTAAGTCAT	43697		

RESULT 8
US-09-949-016-13185/c
? Sequence 13185, Application US/09949016
? Patent No. 6812339
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL0013307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13185
? LENGTH: 251769
? TYPE: DNA
? ORGANISM: Human
US-09-949-016-13185

	Query Match	11.7%	Score 30.6;	DB 4;	Length 251769;
	Best Local Similarity	52.8%	Pred. No. 34;		
	Matches	66;	Conservative	0;	Mismatches 59;
					Indels 0;
					Gaps 0;
Qy	36	GTGTCATGCTTGTGAGAGAGAAAACATCTTCGAGTCGCCAGAACCCAGGAGGTGCAAAATG	95		
Db	218276	GTATCTTGTATCATACAGATATACTATTTTCAGACGAAGAAGAGAGGGGACAAATAA	218217		
Qy	96	GACAGACCCATACCTGCGTTATAGCGGCGGTGAAAAATATTTCCACGTTTTTTTCATCGTTCTG	155		
Db	218216	CAAAGAGTAGTCTGCATAAATGAGGCAATAACTAGTTTCTCTTTTGGCATCAGGAAG	218157		
Qy	156	CAACA 160			
Db	218156	AAACA 218152			

```

RESULT 9
US-09-349-016-13186/c
; Sequence 13186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14

```

;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13186
;; LENGTH: 251769
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13186

Query Match 11.7%; Score 30.6; DB 4; Length 251769;
Best Local Similarity 52.8%; Pred. No. 34;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GTGTCATGCTTGTGAGAGAGAAACACTTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATG 95
DB 218276 GTATCTTGATTCATACAGATATACTATTTTTCAGAGCAAGAAAGAGAGGGGACAAATAA 218217

QY 96 GACAGAGCCATCTCGTTTATAGCGCGGTGAAAAATATTTCCACGTTTTTTTCATGGTTTCG 155
DB 218216 CAAAGAGTAAGTCTGCATAAATGGAGCAATACTAGTTTCTTTTGGCCATGAGAAG 218157

QY 156 CAACA 160
DB 218156 AAACA 218152

RESULT 10
US-09-949-016-13187/c
;; Sequence 13187, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13187
;; LENGTH: 266748
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13187

Query Match 11.7%; Score 30.6; DB 4; Length 266748;
Best Local Similarity 52.8%; Pred. No. 35;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GTGTCATGCTTGTGAGAGAGAAACACTTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATG 95
DB 218241 GTATCTTGATTCATACAGATATACTATTTTTCAGAGCAAGAAAGAGAGGGGACAAATAA 218182

QY 96 GACAGAGCCATCTCGTTTATAGCGCGGTGAAAAATATTTCCACGTTTTTTTCATGGTTTCG 155
DB 218181 CAAAGAGTAAGTCTGCATAAATGGAGCAATACTAGTTTCTTTTGGCCATGAGAAG 218122

QY 156 CAACA 160
DB 218121 AAACA 218117

RESULT 11
US-09-949-016-13188/c
;; Sequence 13188, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13188
;; LENGTH: 266748
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13188

Query Match 11.7%; Score 30.6; DB 4; Length 266748;
Best Local Similarity 52.8%; Pred. No. 35;
Matches 66; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GTGTCATGCTTGTGAGAGAGAAACACTTTCGAGTGCCAGAACCCCAAGGAGGTGCAAAATG 95
DB 218241 GTATCTTGATTCATACAGATATACTATTTTTCAGAGCAAGAAAGAGAGGGGACAAATAA 218182

QY 96 GACAGAGCCATCTCGTTTATAGCGCGGTGAAAAATATTTCCACGTTTTTTTCATGGTTTCG 155
DB 218181 CAAAGAGTAAGTCTGCATAAATGGAGCAATACTAGTTTCTTTTGGCCATGAGAAG 218122

QY 156 CAACA 160
DB 218121 AAACA 218117

RESULT 12
US-08-474-169-7
;; Sequence 7, Application US/08474169
;; Patent No. 5851796
;; GENERAL INFORMATION:
;; APPLICANT: Schatz, David G.
;; TITLE OF INVENTION: An Autoregulatory Tetracycline-Regulated
;; System for Inducible Gene Expression in Eucaryotes
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;; STREET: 1100 New York Ave. Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/474,169
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5157 base pairs

```
/
;
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: . both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 502..2184
US-08-474-169-7

Query Match          11.6%; Score 30.4; DB 2; Length 5157;
Best Local Similarity 54.5%; Pred. No. 5.7; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 51;

QY 131 TATTTCCAGCTTTTTCATGTTTGGCAACAGGTGCTCCGCTGGTGTGCGAGCATGGAGA 190
Db 3047 TTGTGCCAACTCATCAATGATATCATGTCGCTCTAGAGCTGCATTAAATGAATC 3106

QY 191 GACCCAGCCAGAGGAGCGGTTTCTCTCTGGAAGAGCCCATGCCCTTCTT 242
Db 3107 GGCACACGCGGGGAGAGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCT 3158

RESULT 13
US-09-949-016-15881
; Sequence 15881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15881
; LENGTH: 87470
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(87470)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15881

Query Match          11.6%; Score 30.4; DB 4; Length 87470;
Best Local Similarity 49.4%; Pred. No. 24; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 81;

QY 91 AAATGACAGAGCCACTACTGCTGTATAGGGCGGTGAATAATTTCCAGTTTTTCATG 150
Db 17392 AAATGTTCAAGTGAATCTAGTTTAACTGCTTGAAGTGTCTTTTGTGTTTTT 17451

QY 151 GTTCGCAACAGGTGCTCCGCTGTTGTGCGAGCATGGAGACCCCAAGCCAGGAGAAG 210
Db 17452 GACACAGGCTCTGCTCTGTGTCGCCAGGCTGGAGTGCAGTGGCACAATCTCAGCTTACTG 17511

QY 211 CGGTTTCTCTGGAGAGCCCATGCCCTTCTTTTACTCTCA 250
Db 17512 CAGCCTCTGCTCCGCCAGGTTTCAAGCAATTTCTCCACCTCA 17551

RESULT 14
US-09-949-016-16066
; Sequence 16066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16066
; LENGTH: 144362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(144362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16066

Query Match          11.6%; Score 30.2; DB 4; Length 144362;
Best Local Similarity 58.2%; Pred. No. 36; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 38;

QY 27 TAGAGTGTGGTGTCTCATGTTCTGTGAGAGAGAAACACTTTCGAGTCCCAAGGAG 86
Db 27633 TTGAATTTGGTGTGTTATGTTTCATGTTAGAGCCCAACAGGATTTACTGTTAGATAGGTAAGGG 27692

QY 87 GTGCAATGCGACAGAGCCCATCTCGTTTATA 117
Db 27693 GTGTAAGAGGAGTCAAGCATACTGTGTAAGA 27723

RESULT 15
US-09-949-016-14033/c
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14033
; LENGTH: 784019
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(784019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033

Query Match          11.6%; Score 30.2; DB 4; Length 784019;
Best Local Similarity 51.1%; Pred. No. 82; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 68;

QY 17 AGGGTGACAATAGAGTGTGGTGTGTCATGCTGTGAGAGAGAGAAACACTTTCGAGTCCCA 76
Db 326015 AGGGTGAAACAAAGAGGTGTAATAATGCTAGAAATTTACCAATCATGACACAGCGTCA 325956
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Qy 77 ACCCAAGGAGTGCAAAATGACAGAGCCATACTGCGTTATAGCGCGCGTGAATAATTTTC 136
Db 325955 AACCAATGAACTCTCATAGGAATATCAATAAAGCATTTCAGAAACACTAAAAATAATTC 325896
Qy 137 CACGTTTTTTCATGGTTTCG 155
Db 325895 CTTCTCCAACTTTTCTCG 325877

Search completed: August 27, 2005, 11:37:10
Job time : 98.5484 secs

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